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:ch\_pp protein - protein database search, using Smith-Waterman algorithm Wed Aug 16 09:32:39 2000; MasPar time 20.12 Seconds 768.349 Million cell updates/sec

Tabular output not generated.

>US-09-416-267-2 (1-223) from US09416267.pep 1738

Title: Description: Perfect Score:

Sequence: 1 MKLHYVAVLTLAILMFLTWL......IGPECIDYGSKTVKCMNCMF 223

Scoring table: PAM 150 Gap 11

Searched:

225878 seqs, 69334122 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: sptremb112

1:sp\_archea 2:sp\_bacteria 3:sp\_fungi 4:sp\_human 5:sp\_invertebrate 6:sp\_mammal 7:sp\_mhc 8:sp\_organelle 9:sp\_bhage 10:sp\_plant 11:sp\_rodent 12:sp\_unclassified 13:sp\_vertebrate 14:sp\_virus

Statistics: Mean 43.035; Variance 77.012; scale 0.559

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

219 8 8 7 6 5 5 4 3 2 1 1 1 1 1 1 1 1 2 1 2 1 1 1 1 1 1 1	Result No.
11111 10000000000000000000000000000000	Score
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414 434 6440 437 633 1360 1360 2466 7266 7266 7267 7267 7267 7267 7267	Length
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0890182 0890182 099182 0924468 092VU3 095612 099756 099756 099756 014022 014022 051758 021281 021281 021281 021281 021281 021281 021281 021281 021281 021281 021281 021281 021281 021281 021281 021281 021281 021281	ID
MATRILIN. 4 PRECURSOR, INTEGRIN BETA-7 SUBUNI INTEGRIN BEOTEIN. INTEGRIN BEOTEIN INTEGRIC REPRESSOR I-M SPECIAL LOBE-SPECIFIC SPIKE GLYCOPROTEIN. CONTAINS SIMILARITY TO PROBABLE CALCIUM-TRAMS SIMILAR TO HYV6A U88. DNAJ-RELAFED PROTEIN. OLFACTORY RECEPTOR 21 SIMILAR TO PHOSPHOLIPA CONNECTIVE TISSUE GROW SIMILAR TO GLYCYL-TRNA CELL SIZE REGULATION P	, <u>p.</u>
4.57e-02 1.26e-01 1.26e-01 1.26e-01 1.26e-01 6.54e-01 6.54e-01 6.54e-01 1.24e+00 1.24e+00 1.24e+00 3.19e+00 3.19e+00 3.19e+00 3.19e+00 2.34e+00 2.34e+00	Pred. No.

RESULT
OB
AC OE
DT 01
DT 01
DT 01

LT 2
089030 PRELIMINARY; PRT; 434 AA.
089030;
01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TREMBLrel. 08, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)

45	44	43	42	41	40	39	38	37	36	35 5	34	ω ω	32	31	30	29	28	27	26	25	24	23	22	21
86	86	87	87	87	87	87	87	87	87	87	87	87	89	88	88	88	88	88	89	89	91	90	90	91
4.9	•	5.0														5.				•		•	5.2	•
		2195				1080	565	413	326	185	68	63	1964	1652	757	619	593	566 :	381	56	1000	931	849	756
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P87643	Q9WA11	Q20462	Q9WQY2	Q9WQX6	090301	Q23089	Q20571	Q69566	008766	Q18180	024095	020702	035442	Q90633	Q21407	Q90051	Q84248	Q62977	043775	020728	053120	095427	Q9XIL5	044418
STRAIN VIENNA ORF5.	LARGE ENVELOPE PROTEIN	SIMILAR TO C. ELEGANS	POLYPROTEIN P194.	POLYPROTEIN P194.	POLYPROTEIN.	ZK742.1 PROTEIN.	HYPOTHETICAL 61.1 KD P	(HHV-6) U1102, VARIANT	Al RECEPTOR 326 AS.	COSMID C25G6.	MTN16 GENE PRECURSOR.	CYTOCHROME OXIDASE I (	NOTCH4.	COMPLEMENT C3 PRECURSO	SIMILARITY TO GLYCEROP	LARGE T ANTIGEN (FRAGM	T-ANTIGEN.	MITOGEN-ACTIVATED ZINC	CYR61 PROTEIN.	CYTOCHROME OXIDASE I (	HYPOTHETICAL 111.5 KD	MCD4P HOMOLOG.	PUTATIVE MEMBRANE-ASSO	SPECIAL LOBE-SPECIFIC
1.09e+01	1.09e+01	8.03e+00	8.03e+00	8.03e+00	8.03e+00	8.03e+00	8.03e+00	8.03e+00	8.03e+00	8.03e+00	8.03e+00	8.03e+00	4.36e+00	5.92e+00	5:92e+00	5.92e+00	5.92e+00	5.92e+00	4.36e+00	4.36e+00	2.34e+00	3.19e+00	3.19e+00	2.34e+00

#### ALIGNMENTS

Q D	Qy Db	M B Q	RESULTATION OF THE STORY OF THE	
331 CVNLIR-QLECSGQVKSDFR 349  :::: :   :   :   175 CMSIHQCKISCESMGASKYR 194	273 WFKIVSFSGVEELSVDEFIVS-TKTLQDEEVAAVLLNMSNCNNANKMEKSGSCSFG-FEE 330	Query Match 5.9%; Score 102; DB 10; Length 417; Best Local Similarity 27.5%; Pred. No. 6.42e-02; Matches 22; Conservative 20; Mismatches 34; Indels 4; Gaps 4;	O64618  OFA618  OFA618	

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RESULT
                                                                                                                               Matches
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Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-SPRAGUE-DAWLEY; TISSUE-SPLEEN;

TIDSWELL M., PACHYNSKI R., WU S.W., QIU S.Q., DUNHAM E., COCHRAN N.,

BRISKIN M.J., KILSHAW P.J., LAZAROVITS A.I., ANDREW D.P.,

BUTCHER E.C., YEDNOCK T.A., ERLE D.J.;

J. IMMUNOL. 0:0-0(0).

-!- FUNCTION: INTEGRINS ARE A LARGE FAMILY OF CELL SURFACE

GLYCOPROTEINS THAT MEDIATE CELL TO CELL & CELL TO MATRIX ADHESION.

-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUL 1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-NOV-1999 (TREMBLrel. 12, Last annotation update)
INTEGRIN BETA-7 SUBUNIT (FRAGMENT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                009182;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VARIANT
VARIANT
                                                                                                                                                                                                                                                                                                                                            EMBL; AF003598; AAB61241.1; -. PROSITE; PS00243; INTEGRIN_BETA; 3.
                                                                                                                                                                                                                                                                                                                  PFAM; PF00362; integrin_B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Signal; Glycoprotein; EGF-like domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00010; ASX_HYDROXYL; PFAM; PF00008; EGF; 4. PFAM; PF00092; vwa; 1.
                                           432 CSESVDSCVSPEGGIC-SGHGDCKCNRCQCLDGYYGALCDQCLGCKSPCEQYRDCAE 487
                                                                                                                                                                                                                                                                          Integrin; Cell adhesion; Transmembrane; Glycoprotein; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEBS Lett. 436:123-127(1998).
EMBL; AJ006140; CAA06890.1; -
HSSP; P00736; IAPQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          matrix proteins.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MATRILIN-4 PRECURSOR, ALTERNATE SPLICE PRODUCT MAT-4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS; PR00453; VWFADOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=C57BL/6J; TISSUE=TOTAL FOETUS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Matrilin-4, a new member
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WAGENER R., KOBBE B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                    31
                                                                                                                         Match 5.9%; Local Similarity 31.6%; Local Similarity 31.6%; nes 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Match 5.9%;
Local Similarity 41.7%;
les 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9 LSL-LLLFLQSWETQLQSAGKDLCAELVHGC--QHLCVNAPGTFYCAC 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
           CASDVSKCLIQELCQCRPGEGNCSCCK-ECM-LCLGALWDECCDCVGMCNP-RNYSD 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LTLAILMEL-TWLPESLSCNKALCASDVSKCLIQELCQCRPGEGNCSC
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                                                                                                                                                                                                                                    640 AA; 69015 MW; 313C3A97 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           434 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22
22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           47944 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PAULSSON M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       of the
                                                                                                                                                   Score 102; DB 11;
Pred. No. 6.42e-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 103; DB 11; I
Pred. No. 4.57e-02;
6; Mismatches 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               G → > E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MATRILIN-4 PRECURSOR, PRODUCT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MATRILIN-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           B29D5E9A CRC32;
                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    matrilin family of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          640 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 434;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ALTERNATE SPLICE
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                                                                                                                      4.
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Best Local S
Matches 1
  Query Match 5.8%;
Best Local Similarity 26.0%;
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                        WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.
CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
JONES M., KERSHAW J., KIRSTEN J., LASTER N., LATREILLE P.,
LIGHTNING J., LLOYD C., KUMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN F.
SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULTON N.,
THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
WAITSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
"12.2 M of contiguous flucleotide sequence from chromosome III of C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KOEHRER K., BEYER A., MEWES H.W., GASSENHUBER C
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ (
EMBL; ALO50275; CAB4376.1; -.
PROSITE; PS01187; EGF CA; 2.
Hypothetical protein; Glycoprotein; EGF-like du
BPQUENCE 417 AA; 44934 MW; 96417E05 CRC32;
                                                                                                                                                                 PROSITE; PS01095; CHITINASE_18; 1. PFAM; PF00704; Glyco_hydro_18; 1.
                                                                                                                                                                                                                        Nature 368:32-38(1994).
EMBL; Z66524; CAA91419.1; -.
HSSP; P27275; IMMC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      O22468; PRELIMINARY;
Q22468; O1-NOV-1996 (TIEMBLEEL 01,
01-NOV-1996 (TIEMBLEEL 12,
01-NOV-1999 (TIEMBLEEL 12,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9Y409
Q9Y409;
01-NOV-1999 (TremBirel. 12,
01-NOV-1999 (TremBirel. 12,
01-NOV-1999 (TremBirel. 12,
                                                                                                                                                                                                                                                                                                         elegans."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          T13H5.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 T13H5.3 PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
HYPOTHETICAL 44.9 KD PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. MEDLINE; 94150718.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human).
Eukaryota; Metazoa; (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (OCT-1995) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                236 WALHHLKCVDIDECGTEGANCGADQFCVNTEGSYECRDCAKACLGCMGA 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7 Match 5.8%;
Local Similarity 28.6%;
local 9 Tarity 28.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SSUE-KIDNEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WLPESLSC-NKALCASDVSKCLIQELCQCRPGEGNC-SCCKECMLCLGA
                                                                                                                Glycosidase.
633 AA; 707
                                                                                                                70746 MW; F23278E2 CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 100; DB 4
Pred. No. 1.26e-
12; Mismatches
Score 100; DB 5;
Pred. No. 1.26e-01;
18; Mismatches 31
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12; M
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .26e-01;
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                                                      Length 633;
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  Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COULSON A.,
  <u>ن</u>
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Best Local
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 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                          016042;
01-NOV-1996 (TrEMBLrel. 01, Crev
01-JAN-1999 (TrEMBLrel. 09, Las:
01-NOV-1999 (TrEMBLrel. 12, Las:
TUMOR NECROSIS FACTOR RECEPTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEDERSPIEL N.A., PALM C.J., CONWAY A.B., CONN L., HANSEN N.F. ALTAFI H., ARAUJO R., HUIZAR L., ROWLEY D., BUBHLER E., DUNN I GONZALEZ A., KREMENETSKAIA I., KIM C., LENZ C., LI J., LIU S. LUROS S., SCHWARTZ J., SHINN P., TORIUMI M., VYSOTSKAIA V.S., WALKER M., YU G., ECKER J., THEOLOGIS A., DAVIS R.W.; Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases. EMBL; ACO05223; AAD10550.1; -. SEQUENCE 1360 AA; 154661 MW; A7040DF1 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
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01-MAY-1999 (TrEMBLrel. 10,
01-MAY-1999 (TrEMBLrel. 10,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9ZVU3
                                                                                                                                                                                                                                   Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1218
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                                                                                                                                            MEDLINE; 91370690.

DEMBIC Z., LOETSCHER H., GUBLER U., PA
BROCKHAUS M., LESSLAUER W.;
"Two human TNF receptors have similar
                                                                                                                                                                                                                                                                                                                                                                                                                                           1274 WFY-TCDSC 1281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Arabidopsis.
                                                                   EMBL; S63368; AAB19824.1; -.
HSSP; P25942; 1CDF;
PROSITE; PS00652; INFR_NGFR_1; 2.
                                                                                                                intracellular, domain sequences.";
Cytokine 2:231-237(1990).
                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                     Q16042
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                           PFAM;
                                                                                                                                                                                                                                                                                                                                                                                                               195
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        136 FLETVNQPHHQNVSVPSNNVHAPYSSDKEHMCTVVYFDDCMSIHQ-CKISCESMGASKYR 194
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                                             PF00020;
NCE 439
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larity 31.9%;
Conservative
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                                                      TNFR_c6;
 5.5%;
                                            46090 MW;
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Score 95;
Pred. No.
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Pred. No. 2.45e-01;
12; Mismatches 29;
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Last annotation updat
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                                             1CE766FB CRC32;
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                                                                                                                                                                          PAN Y.C.,
                                                                                                                                                                                                                                                                                                                                                       439 AA
   6.54e-01;
                  DB 4;
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                  Length
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                                                                                                                                                                                                                                                    Mammalia;
                                                                                                                                                                            GENTZ R.,
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P95612;
O1-MAY-1997 (TrEMBLrel. 03, C
O1-MAY-1997 (TrEMBLrel. 03, L
O1-AUG-1998 (TrEMBLrel. 07, L
NODULATION PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q99750 PRELIMINARY;
Q99750;
Q1-MAY-1997 (TrEMBLrel. 0
01-MAY-1997 (TrEMBLrel. 0
01-NOV-1998 (TrEMBLrel. 0
MYOGENIC REPRESSOR I-MF.
                                                                                                                                                                                                                                                                                                                                                                                      family.";
Cell 86:731-741(1996).
Cell 86:731-741(1996).
FMBL; U78313; AAB39748.1; -.
FMBL; U78313; AAB39748.1; -.
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MICROBIOLOGY 0:0-0(0).
EMBL; U77701; AAB19229.1; -.
EMBL; U77701 AAB; 64012 MW;
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Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHEN C.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE; 96390847.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE-BRAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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                                                                                                                                                                                                     175
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Local Similarity 29.9%;
les 23; Conservation
76 MC 77
                                                                                                                                 22 ESLS-CNKAL-CASDVSKCLIQE--LCQCRPGEGNCSCCK-ECML-CLGALWDECCDCVG 75
                                                                                                                                                                                                                                                                      Local Similarity
les 24; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WLPESLSCNKALCASD-V-SK-CLI-QE-LCQCRPGEGNCSCCK-E-CMLCLGALWDEC 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WVPECLSCG-SRCSSDQVETQACTREQNRICTCRPG-WYCALSKQEGCRLC-APLRK-C 121
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                                                                                                                                                                                                  EFLTLCNIVLDCAT-CGSCSSEDSCLCCCCCGSGECADCDLPCDLDC-GIL-DACCESAD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KRAUT N.,
                                                                                                                                                                                                                                                                  5.4%;
larity 38.7%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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Pred. No. 6.54e-01
21; Mismatches 3
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Last annotation update)
                                                                                                                                                                                                                                                                  Score 94; DB 4; 1
Pred. No. 9.02e-01;
8; Mismatches 20
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Best Local
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EMBL; x80799; CAA56778.1; -.
PFAM; PF01600; Corona_S1; 1.
PFAM; PF01601; Corona_S2; 1.
SEQUENCE 1454 AA; 161129 MW;
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Q66928;
                                            1416 CCCSTGCCGCIGCL-GSCCH--SMCSRRQFENYEPIEKVHV 1453
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SPIKE GLYCOPROTEIN.
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                                                                                                                                                                                                                                                                                                                                                                              STRAIN=79-1683;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Coronaviridae; Coronavirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Viruses; ssRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CASE S.T., COX C.C., ANIDO A.E.;
Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases
EMBL; AF036896; AAB92416.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HOFFMAN R.T., SCHMIDT E.R., CASE S.T.;
"A cell-specific glycosylated silk protein from Chironomus thummi salivary glands. Cloning, chromosomal localization, and characterization of CDMA.";
J. Biol. Chem. 271:9809-9815(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               feline coronavirus
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TISSUE-SALIVARY GLAND:
SCHERBIK S.
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HOFFMAN R.T., SCHM
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Eukaryota; Meoptera; Endopterygota; Diptera; Nematocera;
Chironomoidea; Chironomidae; Chironominae; Chironomus.
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                                                                                                                                   Match 5.4%;
Local Similarity 34.1%;
53 CSCCKECMLCLGALWDECCDCVGMCNPRNYSDTPPTSKSTV 93
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15; Conse
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29.48;
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Pred. No. 1.
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Pred. No.
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RESULT 12
ID Q21281;
AC Q21281;
AC Q21281;
AC Q21281;
AC Q21281;
AC Q21281;
AC Q21281;
DT Q1-NOV-1999 (TTEMBLTel. 01, Cr DT Q1-NOV-1999) (TTEMBLTel. 12, La DT Q1-NOV-1999) (TTEMBLTel. 12, La DT Q1-NOV-1999) (TTEMBLTel. 12, La DT Q1-NOV-1999) (TTEMBLTEL) L3, La DT Q1-NOV-1999) (TTEMBLTEL) L3, La DT Q1-NOV-1999) (TTEMBLT) TO PFAM DO DE C-VALUE-7.1E-56, N-1.

GN MUP-4,
OS CAENOTANDÍTIS elegans.
OC ELWAIYOTA: Rhabditoidea; Rhabb RN [1]
CR ELWAIYOTA: Rhabditoidea; Rhab RN [2]
RR SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA MONDE;
RT "Genome sequence of the nemato investigating biology. The C.
RL Science 282:2012-2018(1998).
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA FAVELLO T.;
RA SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA WATERSTON R.;
SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA WATERSTON R.;
RL SUBMITTED (MAY-1999) to the EM SEQUENCE FROM SEG; 3.
DR PROSTIE; PS01187; EGF_CA; 2.
DR PROSTIE; PS01187; EGF_CA; 2.
DR PRAM; PF010008; EGF; 3.
DR PRAM; PF010008; EGF; 3.
DR PRAM; PF010008; EGF; 3.
DR PRAM; PF01390; SEA; 2.
DR PRAM; PF01390; SEA; 2.
DR SEQUENCE 2100 AA; 229803 MW
  DR CCCCCARROCOCCDD DIC
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Best Local
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                                             EMBL; 297210; CAB10145.1; -. PFAM; PF00122; E1-E2_ATPase;
                                                                                                                                                                                                                                                                     Eukaryota; Fungî; Ascomycota; Archiascomycetes; Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                        Schizosaccharomyces pombe (Fission yeast). Eukaryota; Fungi; Ascomycota; Archiascomycetes;
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PROSITE; PS01187; EGF_CA; 2.
PFAM; PF00008; EGF; 3.
PFAM; PF01390; SEA; 2.
Glycoprotein; EGF-like domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda;
                                                                                                                                                                                             STRAIN-972;
                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                       Schizosaccharomyces.
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                                     ATPASES).
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Pred. No. 9.02e-01
9; Mismatches 1
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DOMAIN: PF00092 (VWA), SCORE=197.4,
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KOSUGE H., ISEGAWA Y., YAMANISHI K.;
"Nucleotide sequence analysis of a 30-
herpesvirus-6B (HHV-6B) genome and str
immediate-early genes.";
Virus Res. 52:1-14(1997).
EMBL; U92288; AAC40337.1; -
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

MEDLINE; 99287316.

NELSON K.E., CLAYTON R.A., GILL S.R., GWINN M.L., DODSON R.J.,

NELSON K.E., CLAYTON K.A.,

HAFT D.H., HICKEY E.K., PETERSON J.D., NELSON W.C., KETCHUM K.A.,

MCDONALD L., UTTERBACK T.R., MALEK J.A., LINHER K.D., GARREST M.M.,

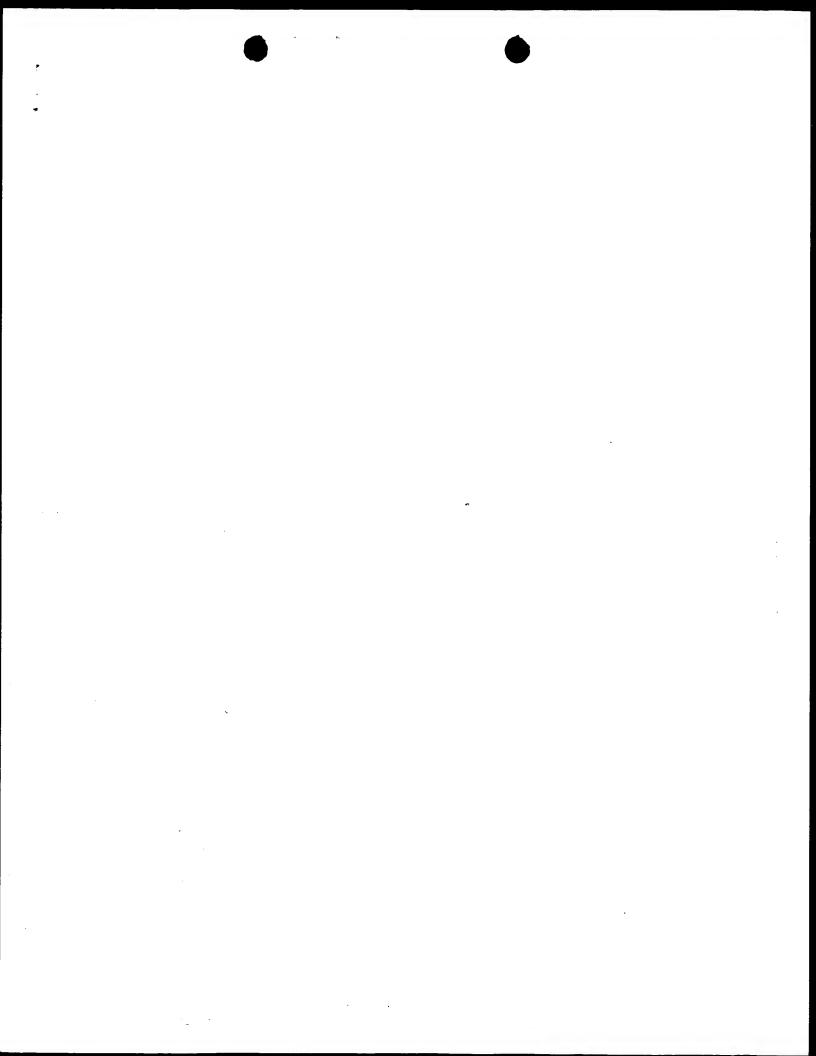
MCDONALD L., UTTERBACK T.R., MALEK J.A., LINHER K.D., RICHARDSON D.,

STEWART A.M., COTTON M.D., PRATT M.S., PHILLIPS C.A., RICHARDSON D.,

STEWART A.M., COTTON G.G., FLEISCHMANN R.D., WHITE O., SALZBERG S.L.,
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MCDONALD L., UTTERBACK T.R., MALEK J.A., LIXHER K.D., GARRETT M.M.,
STEWART A.M., COTTON M.D., PRATT M.S., PHILLIPS C.A., RICHARDSON D.,
HEIDELBERG J., SUTTON G.G., FLEISCHMANN R.D., WHITE O., SALZBERG S.L.,
SMITH H.O., VENTER J.C., FRASER C.M.;
SUDMITTED J.C., FRASER C.M.;
SUDMITTED J.C., FRASER C.M.;
SUDMITTED J.C., FRASER C.M.;
SUDMITTED J.C., FRASER C.M.;
SEMBL, AE001818; AAD3666.1; J. LEGGREG C.G.C.
                                                                                                                                                                                                                                                                                                genome
Nature
[2]
                                                                                                                                                                                                                                                                                                               SMITH H.O., VENTER J.C., FRASER C.M.;
"Evidence for lateral gene transfer between Archaea genome sequence of Thermottoga maritima.";
Nature 399:323-329(1999).
                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
56
                                88
CKECMLCLGALW--DECCD-CVGMCNP
                                CRDILACLGCAWCTDTCCEACGGDCIP 114
                                                               5.2%;
similarity 44.4%;
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Search completed: Wed Aug 16 09:34:37 2000 Job time : 118 secs.



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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

:ch\_pp protein - protein database search, using Smith-Waterman algorithm Wed Aug 16 09:31:40 2000; MasPar time 8.67 Seconds 796.748 Million cell updates/sec

Tabular output not generated.

Title:

Description:
Perfect Score:
Sequence: >US-09-416-267-2 (1-223) from US09416267.pep 1738 1 MKLHYVAVLTLAILMFLTWL.....IGPECIDYGSKTVKCMNCMF 223

Scoring table: PAM 150 Gap 11

Searched: 85661 seqs, 30989116 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: swiss-prot38 1:swissprot

Statistics: Mean 44.527; Variance 72.235; scale 0.616

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	BB	IJ	Description	Pred. No.
٠	537	. :	249	, μ., ;	TSG_DROME	<b>Ω</b> :	
N	104		798	ب	ITB7_HUMAN	INTEGRIN BETA-7 PRECUR	
w	101	5.8	194	ب	COXZ_PARDE	PROBABLE CYTOCHROME C	2.16e-02
4	97		243	μ	GTT2_MOUSE	GLUTATHIONE S-TRANSFER	
տ	97	5.6	806	ш	ITB7_MOUSE	INTEGRIN BETA-7 PRECUR	8.98e-02
σ	97		1799	سر	LMB2_MOUSE	LAMININ BETA-2 CHAIN P	.98e-
7	96		326	<u>س</u> م	AA1R_BOVIN	ADENOSINE A1 RECEPTOR.	1.27e-01
œ	96		446	μ	CLUS_PIG	CLUSTERIN PRECURSOR (C	1.27e-01
9	95	5.5	461	_	TNR2_HUMAN	TUMOR NECROSIS FACTOR	1.80e-01
10	95		471	ب	NOLX_RHIFR	NODULATION PROTEIN NOL	
11	96		1801	_	LMB2_RAT	LAMININ BETA-2 CHAIN P	1.27e-01
12	96	5. 5	3084	լ	LMA1_MOUSE	LAMININ ALPHA-1 CHAIN	1.27e-01
13	94	5.4	62	Н	MT_XENLA	METALLOTHIONEIN.	2.54e-01
14	93	5.4	596	٢	NOLX_RHISN	NODULATION PROTEIN NOL	3.58e-01
15	94	5.4	3075	ш	LMA1_HUMAN	LAMININ ALPHA-1 CHAIN	
16	92	5.3	130	μ.	YKD6_YEAST	HYPOTHETICAL 14.9 KDA	5.02e-01
17	92	5.3	558	ш	GTR2_LEIDO	MEMBRANE TRANSPORTER D	
18	92		1096	щ	ATCY_SCHPO	PROBABLE CATION-TRANSP	5.02e-01
19	90	5.2	63	_	MT1_COLLI	METALLOTHIONEIN-I (MT-	9.81e-01
20	90		167	$\vdash$	Y199_MYCGE	HYPOTHETICAL PROTEIN M	9.81e-01
21	90		324	μ	AA1R_CHICK	ADENOSINE A1 RECEPTOR.	9.81e-01
22	91		445	سر	CLUS_CANFA	CLUSTERIN PRECURSOR (G	7.03e-01
23	90	5.2	690	Н	AFT1_YEAST	IRON-REGULATED TRANSCR	9.81e-01

S

SEQUENCE

249 AA;

27220 MW; 313EE6A406E4B86D CRC64;

Query Match 30.9%; Score 537; DB 1; Length 249; Best Local Similarity 35.4%; Pred. No. 4.07e-100; Matches 79; Conservative 54; Mismatches 71; Indels 19; Gaps 13;

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-	DNA-DIRECTED RNA POLYM	ADENOSINE A1 RECEPTOR.	ADENOSINE A1 RECEPTOR.	HYPOTHETICAL 35.6 KDA	ADENOSINE A1 RECEPTOR	KAPPA CASEIN PRECURSOR	LAMININ ALPHA-5 CHAIN	NEUROGENIC LOCUS NOTCH	STE16 PROTEIN.	HYALURONOGLUCOSAMINIDA	HYPOTHETICAL 102.8 KDA	LARGE T ANTIGEN.	CYR61 PROTEIN PRECURSO	ADENOSINE A1 RECEPTOR.	ADENOSINE A1 RECEPTOR.	ADENOSINE A1 RECEPTOR.	GLUTATHIONE S-TRANSFER	GONADOTROPIN BETA-II C	GONADOTROPIN BETA CHAI	METALLOTHIONEIN 2 (MT-	PLASMA-CELL MEMBRANE G
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### ALIGNMENTS

RESULTANT OF THE PROPERTY OF T	TSG_DROME STANDARD; PRT; 249 AA.  P5435; 01-OCT-1996 (Rel. 34, Careated) 01-OCT-1996 (Rel. 34, Last sequence update) 01-OCT-1996 (Rel. 35, Last annotation update) 01-NOY-1997 (Rel. 35, Last annotation update) TWISTED GASTRULATION PROTEIN PRECURSOR. TSG. Drosophila melanogaster (Fruit fly). Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila. [1] SEQUENCE FROM N.A. TISSUE-EMBRYO; MEDLINE; 95047309. MASON E.D., KONTAG K.D., Webb C.D., Marsh J.L.; "Dorsal midline fate in Drosophila embryos requires twisted gastrulation, a gene encoding a secreted protein related to human connective tissue growth factor."; Genes Dev. 8:1489-1501(1994). Genes Dev. 8:1489-1501(1994).
ខ្លួ	obtile releasement
စ္က ဂ	<pre>melanogaster (Fruit fly). Metazoa; Arthropoda; Tracheata; Hexapoda;</pre>
88	erygota;
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3 2	gene encoding a secreted protein related to
2	Genes Dev. 8:1489-1501(1994).
ဌ	UNCTION: SPECIFY THE FATE OF DORSAL CELLS IN DROSOPHILE
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CC	MIDLINE CELLS AND DO NOT AFFECT DORSAL ECTODERM CELLS.
ဂြ	-!- SUBCELLULAR LOCATION: SECRETED.
2 2	-1- SIMILARITY: SOME, TO THE CEF-10/CYR61/CTFG/FISP-12/NOV PROTEIN FAMILY.
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88	s SWISS-PROT entry is copyright. It is produced through a c
ဌ	en the Swiss Institute of Bioinformatics an
റ്റ	pean Bioinformatics Institute. There are no restrictions on
8	non-profit institutions as long as its content is
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88	ities requires a
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J DR	EMBL; U09808; AAC24234.1;
X C	Developmental protein: Signal.
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collaboration - L outstation -

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MEDLINE; 92135083.

Yuan Q., Jiang W.-M., Krissansen G.W., Watson J.D.;

"Cloning and sequence analysis of a novel beta 2-related integrin transcript from T lymphocytes: homology of integrin cysteine-rich repeats to domain III of laminin B chains.";

Int. Immunol. 3:1373-1374(1991).
                                                                                                                                                           "The gene organization of the human beta 7 subunit, the common be subunit of the leukocyte integrins HML-1 and LPAM-1.";
Int. Immunol. 4:1031-1040(1992).

-i- FUNCTION: EXPECTED TO PLAY A ROLE IN ADHESIVE INTERACTIONS CLEUKOCYTES. INTERACTS WITH ALPHA-4 (TO FORM LPAM-1) OR WITH ALPHA-E (TO FORM HML-1).

ALPHA-E (TO FORM HML-1).

SUBUNIT: DIMER OF AN ALPHA AND BETA SUBUNIT. BETA-7 ASSOCIATIONS OF THE PROPERTY OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Yuan Q., Jiang W.-M., Krissansen G.W., Watson J.D.;
"Cloning and sequence analysis of a novel beta 2-related integrin
transcript from T lymphocytes: homology of integrin cysteine-rich
repeats to domain III of laminin B chains.";
Int. Immunol. 2:1097-1108(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
15-FEB-2000 (Rel. 39, Last annotation updat
INTEGRIN BETA-7 PRECURSOR.
                                                                                                                                                                                                                                                                                                          Jiang W.-M., Jenkins D., Yuan Q., Leung E.,
Krissansen G.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Complete amino acid sequence of an identified in leukocytes.",
J. Biol. Chem. 266:11009-11016(1991).
                                       WITH ALPHA-4 AND -IEL.
SUBSCELULAR LOCATION: TYPE I MEMBRANE PROTEIN.
ALTERNATIVE PRODUCTS: THE DIFFERENT FORMS OF BETA-7 SUBUNIT MAY ARISE BY ALTERNATIVE SPLICING OF PRIMARY MENA TRANSCRIPTS.
TISSUE SPECIFICITY: EXPRESSED IN A VARIETY OF LEUKOCYTE LINES.
PTM: THE CYSTEINE RESIDUES ARE INVOLVED IN INTRACHAIN DISULFIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IRFSMRAGFKQR---V---QG-GAS--GDAGNGNGNAG-SAGVT-LCTVIYVNSCIRA 163
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      TO THE INTEGRIN BETA CHAIN FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Craniata; Vertebrata; Euteleostomi;
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n integrin beta subunit (beta
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                                                                                                                                                                                                                                                                                                                           Watson
                                                                                                                                                               ASSOCIATES
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PROSITE; PS000243; INTEGRIN, BETA; 3.
PROSITE; PS00022; EGE_1; UNKNOWN_1.
PROSITE; PS01186; EGF_2; UNKNOWN_1.
Thtegrin; Cell adhesion; Transmembrane; Glycoprotein; Repeat;
Thtegrin; Cell adhesion; Transmembrane; Signal; Phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PR00362; integrin_B; 1.
PRONTE; PR01186; INTEGRINB.
PROSTITE; PS00243; INTEGRIN BET
PROSTITE:
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                                                                                                                                                                                                    CARBOHYD
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147559; -
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$49365; AAB23668.
$49365; AAB23668.
$49366; AAB23668.
$49367; AAB23668.
$49368; AAB23668.
$49370; AAB23668.
$49371; AAB23668.
$49371; AAB23668.
$49373; AAB23668.
$49374; AAB23668.
$49374; AAB23668.
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M62880; AAA59185.1;
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798
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                                                                                               POTENTIAL.
PHOSPHORYLATION (BY TYR-KINASES)
(BY SIMILARITY).
Score
Pred.
                                                                            MISSING
                                                                                                                                                                                                                                                                                                                                                                          CYSTEINE-RICH REPEATS
                                                                                                                                                                                                                                                                                                                                                                                             INTEGRIN BETA-7.
EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
                                                     BY SIMILARITY).
ISSING (IN SHORT ISOFORM
CBE275E0E9992385 CRC64;
104; DB 1;
No. 7.22e-03;
                Length 798;
                                                                        ISOFORM)
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SEQUENCE FROM N.A.
MEDLINE; 91190778.
Yuan Q., Jiang W.-M.,

REVISIONS

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58 Н

MKLH-YVAVLTLAILMELTWLPESLSCNKALCASDVSKCLIQELCQCRPGEGNCSCCKEC

59 57

MQLLCYFVILFVGIAPW-SSLANDDGCNEVVCGSVVSKCLITQSCQCKLND--CHCCKDC

RESULT

ITB7

HUMAN

STANDARD;

Eukaryota;

Metazoa;

ITGB7

Mammalia; Eutheria; Homo sapiens (Human)

Primates; Chordata;

MEDLINE; 91250405.

EQUENCE FROM N.A.

SSUE-LEUKOCYTE;

CCCCCCCCCCCRARRARARA

BONDS. SIMILARITY: BELONGS

SEQUENCE FROM N.A. MEDLINE; 93002753.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL;
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Mus musculus (Mouse).
Mus musculus (Mouse).
Chordata;
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15-FEB-2000
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                              Whittington A.T.,
                                                          STRAIN=129/SV, AND MEDLINE; 96207306.
                                                                                                                                                                           Mammalia; Eutheria; Rodentia;
                                                                                                                    SEQUENCE FROM N.A.
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Whittington A.T., Webb G.C., Baker R.T., Board P.G.; ^{\circ}Characterization of a cDNA and gene encoding the mouse theta class
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 FPVAEELSHHENLVSFLETVNQPHHQNVSVPSNNVHAP 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      81 MOREMELKIGENAIAFYEAINNTDEPVTGTASYNV-AP 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63 LGAL-WDECCDCVGMCNPRNYSDTPPTSKSTVEE-LHEPIPSLFRALTEGDTQLNWNIVS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23 MGALSWAAVPFYSWFCKVTGFAGTTNVAEAASDTVLDEKIRVRF-D-ANADSNLGWTFRP 80
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Local Similarity 25.5%;
les 25; Conservation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FUNCTION: PROBABLY EXERTS ITS EFFECT AT SOME TERMINAL STAGE OF ENZYME SYNTHESIS, PERHAPS IN DIRECTING ASSEMBLY OF THE SUBUNITS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; X05828; CAA292
S03806; S03806.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       194 AA;
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(Rel. 08, Last sequence update)
(Rel. 39, Last annotation update)
TOCHROME C OXIDASE ASSEMBLY PROTEIN
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                                                                                     AND B6/CBA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    33 P
21325 MW;
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                                                                                  TISSUE-LIVER;
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Pred. No. 2.16e-02;
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                                                                                                                                                                                                       Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                        Sciurognathi;
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                                                                                  SEQUENCE
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                                                          MEDLINE;
                                                                                                                                                Mammalia;
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23; Conse
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                                                                                                                                             Eutheria;
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llarity 32.9%;
Conservative
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Rodentia;
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RRR COC OC DTT DTT
Hu M.C.T. "Cloning
                                                                                                                                                                                                                  P26011; Q64656;
01-MAY-1992 (Rel. 22, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
INTEGRIN BETA-7 PRECURSOR (INTEGRIN BETA-P) (M290 IEL ANTIGEN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OF EXOGENOUS AND ENDOGENOUS HYDROPHOBIC -!- CATALYTIC ACTIVITY: RX + GLUTATHIONE -!
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mainwaring G.W., Williams S.M., Foster J.R., Tugwood J., Green T.; "The distribution of theta-class glutathione S-transferases in the liver and lung of mouse, rat and human."; Biochem. J. 318:297-303(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          92 TVEELHEPIPSLFRALTEGDTQLN-W-NIV-SFPVAEELSHHENLVSFLETVNQPHHQNV 148
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TISSUE SPECIFICITY: IN LIVER, HIGHEST EXPRESSION FOUND IN CENTRI
VEIN LIMITING PLATE HEPATOCYTES. ALSO EXPRESSED IN INTERLOBULAR
BILE DUCT EPITHELIAL CELLS. IN LUNG, EXPRESSED IN CLARA CELLS AL
CILIATED CELLS OF THE BRONCHIOLAR EPITHELIUM AND IN TYPE II
ALVEOLAR CELLS OF THE LUNG PARENCHYMA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY: BELONGS TO THE GST SUPERFAMILY. THETA FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SLEELMOPV-GLGYNLFEGRPQLTAWRERVEAF-LGAEL-YQEAHSTILSILGQAAKKML
and expression of mouse integrin beta
                     Crowe D.T., Weissman I.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Multigene family; Nuclear protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE-LIVER, AND LUNG
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Pred. No. {
19; Mismat
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S -> R (IN STRAIN 129/SV).

G -> A (IN STRAINS 129/SV ANT
Y -> C (IN STRAINS 129/SV ANT
AG: AG97D35B59342726 CRC64;
                                                                                                                      Craniata; Vertebrata;
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                        PRT;
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                                                                                                                                                                                                                                                                                                                                                        806 AA
                       Holzmann
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p(beta 7):
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                                                                                                                                                                                                                                                                                  EMBL; M68903; AAA02749.1; --
EMBL; M95632; AAA39323.1; --
EMBL; M95633; AAA39324.1; --
EMBL; S44607; AAB33193.1; --
EMBL; S63504; AAB27396.1; --
                                                                                                                    PROSITE; PS00243; PROSITE; PS00022; PROSITE; PS01186;
                                                                                                                                                                                                                                                                                                                                                                                  or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    <del>:</del>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Yuan Q., Jiang W.-M., Hollander D., Leung Krissansen G.W.; "Identity between the novel integrin beta
                                                          CHAIN
                                                                        SIGNAL
                                                                                                                                                                        PRINTS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Krissansen G.W.;
"The mouse beta 7 integrin gene promoter: transcriptional regulation of the leukocyte integrins LPAM-1 and M290.";
Int. Immunol. 5:551-558(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Biochem.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SIMILARITY: BELONGS TO THE INTEGRIN BETA CHAIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE; 93305607.
Leung E., Mead P.E., Yuan Q., Jiang W.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE;
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"Molecular cloning of the mouse integrin beta 7 subunit.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 1-67 FROM N.A.
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intestine.";
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. Immunol. 149:1964-1972(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Expression of murine beta 7, alpha 4, and beta 1 integrin genes by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Molecular cloning of the mouse integrin beta 7 subunit.", Biol. Chem. 267:7352-7358(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WITH ALDHA-4 AND -IEL.
WITH ALDHA-4 AND -IEL.
SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 . Immunol. 5:551-558(1993).
FUNCTION: A COMPONENT OF THE PEYER'S PATCHES-SPECIFIC HOMING RECEPTOR AND IS INVOLVED IN ADHESIVE INTERACTIONS OF LEUKOCYTES SUBUNIT: DIMER OF AN ALPHA AND BETA SUBUNIT. BETA-7 ASSOCIATES
                                                                                                                                                                                                                                    PN0017;
A46271;
A42483;
                                                                                                                                                                                                       MGI:96616;
                                                                                                                                                                    PF00362; integrin_B; 1.
S; PR01186; INTEGRINB.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OF 1-90 FROM N.A., AND SEQUENCE OF 91248239.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Biophys. Res. Commun. 176:1443-1449(1991).
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                                                                                                                                                                                                                                                   PN0017.
A46271.
                                                                                                                                                                                                                                     A42483.
                                                                                                   243; INTEGRIN_BETA; 3.
022; EGF_1; UNKNOWN_4.
186; EGF_2; UNKNOWN_1.
1 adhesion; Transmembra
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                                                                                    Cytoskeleton;
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                                                                                Transmembrane; Glycoprotein; Repeat; toskeleton; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                intraepithelial lymphocytes
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.A. 89:8254-8258(1992).
 EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
                                                     INTEGRIN BETA-7
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                                                                             Noakes P.G., Gautam M., Mudd J., Sanes J.R., Merlie J.P.;
"Aberrant differentiation of neuromuscular junctions in mice lacking s-laminin/laminin beta 2.";
Nature 374:258-262(1995).
"Interestable of the ATTACHMENT, MIGRATION, & ORGANIZATION CONTROL TISTHOUGHT TO MEDIATE THE ATTACHMENT, MIGRATION, & ORGANIZATION CONTROL TISTHOUGHT TO MEDIATE THE ATTACHMENT, MIGRATION, & ORGANIZATION CONTROL TISTHOUGHT TO MEDIATE THE ATTACHMENT, MIGRATION & ORGANIZATION CONTROL TISTHOUGHT TO MEDIATE THE ATTACHMENT, MIGRATION, & ORGANIZATION CONTROL TISTHOUGHT TO MEDIATE THE ATTACHMENT, MIGRATION BY INTERACTING CELLS INTO TISSUES DURING EMBRYONIC DEVELOPMENT BY INTERACTING
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                                                                                                                                                                                                                                                                                                                                                                                              genes, and alternative splicing at the transcript.";
                                                                                                                                                                                                                                                                                                                                                                                                                                             Durkin M.E., Gautam M., Loechel Albrechtsen R., Wewer U.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse)
                                                                                                                                                                                                MEDLINE; 95191650.
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                                  NERVE TERMINALS.
                                                WITH OTHER EXTRACELLULAR MATRIX FUNCTION: LAMININ-3 (S-LAMININ)
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LAMININ IS A COMPLEX GLYCOPROTEIN, CONSIST POLYPEPTIDE CHAINS (ALPHA, BETA, GAMMA),
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PROSITE; PS01186; EGF_2; 2.
PROSITE; PS01248; LAMININ_TYPE_EGF;
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PF00055; laminin_Nterm; 1
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Bovidae; Bovinae; Bos.
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Tucker A.L., Linden J., Robeva A.S., D'Angelo D.D., Lynch "Cloning and expression of a bovine adenosine Al receptor FEBS Lett. 297:107-111(1992).
                                                                    SEQUENCE FROM N.A.
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                                        MEDLINE; 92201360.
                                                       TISSUE-BRAIN;
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1 RECEPTOR.
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15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
CLUSTERIN PRECURSOR (COMPLEMENT CYTOLYSIS INHIBITOR) (CLI).
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G-protein coupled receptor; Transmembrane; Glycoprotein;
Lipoprotein; Palmitate,
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1 10 EXTRACELLULAR (POTENTIAL).

TRANSMEM 11 33 1 (POTENTIAL).
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SEQUENCE FROM N.A.
MEDLINE; 92268130.
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                                                                                                                                                                           Local
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                                                                                                                                     LALILELFALSWLPLHILNCITLFCPSCHMPRILI 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         $22213; $22213.
$20390; $20390.
                                                                                                              LTLAILMF-LTWLP-ESLSCNKALCAS-DVSKCLI 40
                                                                                                                                                                          Similarity
                                                                                                                                                                                                               326
                                                                                                                                                                 Conservative
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                                                                                                                                                                                                               AA;
                                                               STANDARD;
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                                                                                                                                                                                                               MW;
                                                                                                                                                                        Score 96; DB 1;
Pred. No. 1.27e-01
                                                                                                                                                             11; Mismatches
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M -> I (IN REF. 2).
; 1697A5F303A57285 CRC64;
                                                                                                                                                                                                                                                                                 7 (POTENTIAL)
CYTOPLASMIC ()
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7 (POTENTIAL)
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OCCUPATOR
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Best Local
        TNR2_HUMAN STANDARD; PRT; 461 AA.

P2033;

01-FEB-1991 (Rel. 17, Created)

01-AUG-1991 (Rel. 19, Last sequence update)

15-FEB-2000 (Rel. 39, Last annotation update)

TUMOR NECROSIS FACTOR RECEPTOR 2 PRECURSOR (TUMOR NECROSIS FACTOR
BINDING PROTEIN 2) (TBPII) (P80) (TNF-R2) (P75) (CD120B) (ETANERCEPT).

TNFRSF1B OR TNFR2 OR TNFBR.
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CARBOHYD
CARBOHYD
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CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AND HYDROPHOBIC PROTEINS. IT HAS BEEN ASSOCIATED WITH PROGRAMMED CELL DEATH (BY SIMILARITY).

-!- SUBUNIT: ANTIPARALLEL DISULFIDE-LINKED HETERODIMER (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      in vitro.
J. Biol. (
                                                                                                                                                                                                                                                                                                                                                    CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00492; CLUSTERIN_1; PROSITE; PS00493; CLUSTERIN_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; M84639; AAA31013.1; -.
PFAM; PF01093; Clusterin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIGNAL
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                                                                                                                                                                      112 TQLNWNIVSFPVAEELSHHENLVSFLETVNQPHH 145
                                                                                                                                                                                               223 SRFARNIMPFPLFTDLNYHDMFQPFFDMIHQAQQ 256
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9101. Chem. 267:5257-5264(1992).

FUNCTION: NOT YET CLEAR, IT IS KNOWN TO BE EXPRESSED IN A VARIETY OF TISSUES AND IT SEEMS TO BE ABLE TO BIND TO CELLS, MEMBRANES,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE SPECIFICITY:
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larity 23.5%;
Conservative
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ALPHA-CHAIN (B CHAIN).
INTERCHAIN (BY SIMILARITY).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi

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Beltinger C.P., White P.S., Maris J.M., Sulman Lepaslier D., Stallard B.J., Goeddel D.V., Dess Brodeur G.M.;

"Physical mapping and genomic structure of the cenomics 35:94-100(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kohno T., Brewer M.T., Baker S.L., Schwartz P.E., King M.W., Hale K.K., Squires C.H., Thompson R.C., Vannice J.L.; "A second tumor necrosis factor receptor gene product can shed naturally occurring tumor necrosis factor inhibitor."; proc. Natl. Acad. Sci. U.S.A. 87:8331-8335(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cellular and viral proteins.";
Science 248:1019-1023(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Smith C.A., Davis T., Anderson D., Solam L., I
Dower S.K., Cosman D., Goodwin R.G.;
"A receptor for tumor necrosis factor defines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE; 90349972.
Heller R.A., Song K., Onasch M.A., Fischer W.H., Chang
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[1]
                                                                                                                                                                                                                                                                                               Pennica D., Lam V.T., Mize N.K., Weber R.F., Lewis M., Fendly B.M., Lipari M.T., Goeddel D.V.;
"Blochemical properties of the 75-kDa tumor necrosis factor recepto Characterization of ligand binding, internalization, and receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Loetscher H., Schlaeger E.J., Lahm H.-W., Brockhaus M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      urine. Evidence for immunological cross-reactivity with cell surface tumor necrosis factor receptors.";
J. Biol. Chem. 265:1531-1536(1990).
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                                                                                                                                                                                           MEDLINE; 99221490.
Park Y.C., Burkitt V.,
                                                                                                                                                                                                                                                                                                                                                                                                                          "Purification and partial amino acid sequence analysis of two distinct tumor necrosis factor receptors from HL60 cells."; J. Biol. Chem. 265:20131-20138(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE: 90110215.
Engelmann H., Novick D., Wallach D.;
"Two tumor necrosis factor-binding proteins purified from human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
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                                                                                                                                           Nature 398:533-538(1999).
                                                                                                                                                          "Structural basis for self-association human TRAF2.";
                                                                                                                                                                                                                                                                              pnosphorylation.";
                                                                                                                                                                                                                                                                                                                                                                          MEDLINE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Complementary DNA cloning of a receptor for tumor necrosis factor and demonstration of a shed form of the receptor."; proc. Natl. Acad. Sci. U.S.A. 87:6151-6155(1990).
                                                                                                                                                                                                                                x-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 419-428 IN TRAF2 COMPLEX
                                                                                                                                                                                                                                                                   Biol.
                                                                    FUNCTION: RECEPTOR FOR TWF-ALPHA. HIGH AFFINITY FOR TWA-ALPHA AND APPROXIMATELY 5-FOLD LOWER AFFINITY FOR TWF-BETA.
SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
PTM: PHOSPHORYLATED; MAINLY ON SERINE RESIDUES WITH A VERY LOW
LEVEL ON THREONINE RESIDUES.

PHARMACEUTICAL: AVAILABLE UNDER THE NAME ENBREL (IMMUNEX AND WYETH-AYERST). USED TO TREAT MODERATE TO SERVERE RHEUMATOID ARTHRITIS (RA). ENBREL CONSIST OF THE EXTRACELLULAR LIGAND-BINDING
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91056048.
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                                                                                                                                                                     g L., Wu H.;
and receptor recognition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              of the human TNFR2 gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pan Y.-C.E., Lesslauer
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Desauvage F.J.,
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the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                   PORTION OF THER2 LINKED TO AN IMMUGLOBULIN FC CHAIN. IT BINITER-ALPHA AND BLOCKS ITS INTERACTIONS WITH RECEPTORS.

-!- SIMILARITY: CONTAINS A LA-NGER/TWER-TYPE CYSTEINE-RICH REGIONING AND A LA-NGER/TWER-TYPE CYSTEINE-RICH REGIONING NOTE-CD Guide CD120b entry;

WWW-"http://www.ncbi.nlm.nih.gov/prow/cd/cd120b.htm".

-!- DATBABSE: NAME=Enbrel; NOTE-Clinical information on Enbrel;

WWW-"http://www.enbrelinfo.com/".
                                                                                                         This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the El
                                     There are no restrictions ong as its content is in
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Matches 25; Conser
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EMBL; U52164; AAC50622.1
EMBL; W55994; AAA36755.1
PIR; A35356; A35356.
PIR; A36007; A36007.
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EMBL; U52160;
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PROSITE; PS50050; TNFR_NGFR_2; 4.
Receptor; Transmembrane; Glycoprotein; Repeat; Signal; Phosphorylation; Pharmaceutical; 3D-structure.
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REPEAT
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Conservative
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Score 95; DB 1; 1
Pred. No. 1.80e-01
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POTENTIAL.
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STANDARD;

RESULT RE

NOLX

NODULATION PROTEIN NOLX.

Plasmid

sym.

Bacteria; Proteobacteria;

Rhizobiaceae;

Sinorhizobium

STRAIN-USDA 257 SEQUENCE FROM N.A.

MEDLINE; 94018604.

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01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
LAMININ BETA-2 CHAIN PRECURSOR (S-LAMININ)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; L12251; AAB17674.1; ALT_SEQ. PIR; S35019; S35019. Plasmid; Nodulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Meinhardt L.W., Krishnan H.B., Balatti P.A., Pueppke S.G.;
"Molecular cloning and characterization of a sym plasmid locus
regulates cultivar-specific nodulation of soybean by Rhizobium
USDA257."
Mol. Microbiol. 9:17-29(1993).
-i- FUNCTION: REGULATES CULTIVAR-SPECIFIC NODULATION OF SOYBEAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
15-FEB-2000 (Rel. 39, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                    156 PSTPPDLKAAIEALLQD-PELFYAIGSQGDGRCGGKITAKDLSEFSKHHPQVAAFQESQA 214
                                                                                                                                                                                                                                                                                                                                                                                     83 SDTPPTSKSTVEELHEPIPSLFRAL-TEGDTQLNWNIVSFPVAEELSHHENLVSFLETVN 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                . Microbiol. 9:17-29(1993).
FUNCTION: REGULATES CULTIVAR-SPECIFIC NODULATION OF SOYBEAN.
DEVELOPMENTAL STAGE: EXPRESSED CONTINUOUSLY FROM PREINFECTION
THE STAGE OF THE FUNCTIONAL NODULE.
INDUCTION: BY FLAVONOID SIGNAL COMPOUNDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SWISS-PROT entry is copyright. It is produced through
sen the Swiss Institute of Bioinformatics and the EM
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Pred. No. 1.80e-0.
21; Mismatches
                         J.P.,
                                                                                                         Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rat
                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                     otation update)
(S-LAMININ) (LAMININ CHAIN
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                         Sanes J.R.;
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      CHARGE ON THE CONTAINS

CHARGE IN CONSISTING OF THREE

CONTRIBERNY POLYPEPTIDE CHAINS (ALPHA, BETA, GAMMA), WHICH ARE BOUND

CHO EACH OTHER BY DISULFIDE BONDS INTO A CROSS-SHAPED MOLECULE

COMPRISING ONE LONG & THREE SHORT ARMS WITH GLOBULES AT EACH END.

CHE BETA-2 CHAIN IS A SUBUNIT OF LAMININ-3 (S-LAMININ), LAMININ-4

(S-MEROSIN), AND LAMININ-7 (KS-LAMININ).

CHO SECELLULAR LOCATION: EXTRACELLULAR.

CHO SECELLULAR LOCATION: EXTRACELULIDAR.

CHO SECELLULAR JUNCTION.

CHO SECELLULAR LOCATION: EXTRACELULIDAR.

CHO DOMAIN: THE ALPHA-HELICAL DOMAINS I AND II ARE THOUGHT TO INTERACT WITH OTHER LAMININ CHAINS OF FORM A COILED COIL STRUCTURE.

CHO SIMILARITY: CONTAINS I LAMININ DOMAIN DOMAIN (DOMAIN VI).

CHO SIMILARITY: CONTAINS I LAMININ DOMAIN IV.
                 DOMAIN
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Nature 338:229-234(1989).

-!- FUNCTION: BINDING TO CELLS VIA A HIGH AFFINITY RECEPTOR, LAMININ IS THOUGHT TO MEDIATE THE ATTACHMENT, MIGRATION, & ORGANIZATION C CELLS INTO TISSUES DURING EMBRYONIC DEVELOPMENT BY INTERACTING WITH OTHER EXTRACELLULAR MATRIX COMPONENTS.
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                                                                                                                     DOMAIN
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PROSITE; PS01186; EGF_2; 2.
PROSITE; PS01248; LAMININ_TYPE_EGF; 12.
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HSSP; P02468; 1KLO.
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PF00055; laminin_Nterm; 1
S; PR00011; EGFLAMININ.
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1146
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DOMAIN II.

DOMAIN ALPHA.

DOMAIN I.

DOMAIN I.

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COILED COIL (POTENTIAL).

COILED COIL (POTENTIAL).

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BY SIMILARITY.

BY SIMILARITY.
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LAMININ EGF-LIKE 2.
LAMININ EGF-LIKE 3.
LAMININ EGF-LIKE 5 (INCOMPLETE).
LAMININ EGF-LIKE 5 (INCOMPLETE).
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LIKE REPEATS (DOMAIN
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RESULT AC PLANT OF THE PROPERTY OF THE PROPERT

Chordata; Rodentia;

MEDLINE; 89159410.
Hunter D.D., Shah V., Mer
A laminin-like adhesive

Merlie

TISSUE-LIVER; SEQUENCE FROM N.A. Eukaryota; Metazoa; Mammalia; Eutheria; Rattus norvegicus (Rat). Ϋ́

142

OSYAONY-IPSDSAENA 230 QPHHQNVSVPSNNVHAP 158

LMB2\_RAT P15800;

STANDARD;

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Query Match Best Local S Matches 2

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      Mammalia; [1]
                                                LMAI_MOUSE STANDARD; PRT; 3084 AA.
P19137;
01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
LAMININ ALPHA-1 CHAIN PRECURSOR (LAMININ A CHAIN).
LAMA1 OR LAMA-1 OR LAMA.
                                                                                                                                                                                1041 CTCNLLGTDPQRCPSTDLCHCDPSTGQCPC 1070
                Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                       Mus musculus (Mouse)
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Rodentia;
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INTERCHAIN (PROBABLE).
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                Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                       Y SIMILARITY
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    EMBL; J04064; AAA39410.1; -
EMBL; X07737; CAA30561.1; -
EMBL; X19459; CAA31807.1; -
EMBL; M36775; AAA39406.1; -
PIR; A31771; MMMSA.
                                                                                                                                   PFAM;
PFAM;
PFAM;
PFAM;
                                                                                                                                                                                                                                                                                                                                                                                                                                             EUI. J. Blochem. 177:35-45(1988).

-!- FUNCTION: BINDING TO CELLS VIA A HIGH AFFINITY RECEPTOR, LAMININ IS THOUGHT TO MEDIATE THE ATTACHMENT, MIGRATION, & ORGANIZATION OF CELLS INTO TISSUES DURING EMBRYONIC DEVELOPMENT BY INTERACTING WITH OTHER EXTRACELLULAR MATRIX COMPONENTS.

-!- SUBUNIT: LAMININ IS A COMPLEX GLYCOPROTEIN, CONSISTING OF THREE SUBUNITY CHAIN IS A COMPLEX GLYCOPROTEIN, CONSISTING OF THREE DUND TO EACH OTHER BY DISULFIDE BONDS INTO A CROSS-SHAPED MOLECULE COMPRISING ONE LONG & THREE SHORT ARMS WITH GLOBULES AT EACH END. THE ALPHA-1 CHAIN IS A SUBUNIT OF LAMININ-1 (EHS LAMININ) AND LAMININ-3 (S-LAMININ).

-!- SUBCELLULAR LOCATION: EXTRACELLULAR.

-!- TISSUE SPECIFICITY: FOUND IN THE BASEMENT MEMBRANES (MAJOR
                        CHAIN
MOD_RES
DOMAIN
                                                                                                                                                                                        EMBL;
PIR; P
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                                                                                                                                                                                                                                                                use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fc entitles requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
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                                                                                       PROSITE; PS00022; EGF_1; 11.
PROSITE; PS01186; EGF_2; 3.
PROSITE; PS01248; LAMININ_TYPE_EGF; 15.
                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Enthe European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hartl L., Oberbaeumer I., Deutzmann R The N terminus of laminin A chain is Eur. J. Biochem. 173:629-635(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     domain and homology with laminin B chains.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sasaki M., Kleinman H.K., Huber H., Deutzmann R., Yamada Y.; "Laminin, a multidomain protein. The A chain has a unique globular domain and homology with the basement membrane proteoglycan and the
                                                         SIGNAL
                                                                                                                                                                                MGD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Structural study of long arm fr
repetitive C-terminal sequences
chains.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 1-339 FROM N.A. MEDLINE; 88225080. Hartl L., Oberbaeumer I., D
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                                                                    31ycoprotein;
Laminin EGF-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Deutzmann R.,
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                                                                                                                                 M; PF00052; 1
M; PF00053; 1
M; PF00054; 1
M; PF00055; 1
                                                                                                                                                                                                                                                                                                                                                    COMPONENT).

COMPONENT): THE ALPHA-HELICAL DOMAINS I AND II ARE THOUGHT TO INTERACT DOMAIN: THE ALPHA-HELICAL DOMAINS I AND II ARE THOUGHT TO INTERACT WITH OTHER LAMININ CHAINS TO FORM A COILED COIL STRUCTURE.

DOMAIN: DOMAINS VI, IV AND G ARE GLOBULAR.

SIMILARITY: CONTAINS 1 LAMININ TERMINAL DOMAIN (DOMAIN VI).

SIMILARITY: CONTAINS 17 LAMININ BEF LIKE DOMAINS.

SIMILARITY: CONTAINS 2 LAMININ DOMAINS IV.
                                                                    EGF-like domai
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                                                                                                                                laminin_EGF; 15.
laminin_G; 5.
laminin_Nterm; 1.
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                                                                   domain;
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3084
25
276
519
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long arm fragments of laminin. Evidence for
l sequences in the A-chain, not present in t)
                                                                 membrane; Extracellular matrix;
n; Cell adhesion; Repeat; Signal
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LAMININ ALPHA-1 CHAIN.
BLOCKED.
LAMININ N-TERMINAL (DOMAIN VI).
4.5 X LAMININ EGF-LIKE REPEATS
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797
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908
957
1004
11050
11156
11166
11368
        LAMININ EGF-LIKE 9.

LAMININ EGF-LIKE 10.

LAMININ EGF-LIKE 11.

LAMININ EGF-LIKE 12.

LAMININ EGF-LIKE 13.

LAMININ EGF-LIKE 14 (C-TER

LAMININ EGF-LIKE 14 (C-TER

LAMININ EGF-LIKE 15.

LAMININ EGF-LIKE 16.

LAMININ EGF-LIKE 17.

DOMAIN II AND I.

5 X LAMININ EGF-LIKE REPEATS

LAMININ EGF-LIKE 17.

DOMAIN I AND I.

5 X LAMININ G-LIKE 1.

LAMININ G-LIKE 1.

LAMININ G-LIKE 2.

LAMININ G-LIKE 3.

LAMININ G-LIKE 1.

LAMININ G-LIKE 2.

LAMININ G-LIKE 1.

LAMININ G-LIKE
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MININ EGF-LIKE 2.

MININ EGF-LIKE 3.

MININ EGF-LIKE 5 (N-TERMINAL).

MININ EGF-LIKE 5 (DOMAIN IV B).

X LAMININ EGF-LIKE REPEATS (DOMAIN
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IN EGF-LIKE 7.

IN EGF-LIKE 8.

IN EGF-LIKE 9.

IN EGF-LIKE 11.

IN EGF-LIKE 11.

IN EGF-LIKE 12.

IN EGF-LIKE 13.

IN EGF-LIKE 13.

IN EGF-LIKE 14 (N-TERMINAL).

IN DOMAIN IV 2 (DOMAIN IV A).

LAMININ EGF-LIKE REPEATS (DOMAIN).
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01-NOY-1997 (Rel. 3.
METALLOTHIONEIN.
MT-A.
        SEQUENCE FROM N.A.
TISSUE=LIVER;
MEDLINE; 93263990.
St Jacques E., Seguin C.;
"Cloning and nucleotide se
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Q05890;
Q1-FEB-1994
Q1-FEB-1994
Q1-NOV-1997
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                                                                            Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniat
Amphibia; Batrachia; Anura; Mesobatra
Xenopodinae; Xenopus.
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Similarity 37.5%;
15; Conservative
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, Last sequence up
, Last annotation
           sequence of a complementary DNA encoding
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                                                                                                  Mesobatrachia; Pipoidea; Pipidae;
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Pred.
6; M
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POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                            96;
                                                                                                                 lata; Vertebrata; Euteleostomi;
                                                                                                                                                                                 update)
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Best Local Similarity 44.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Muller J.-P., Wouters-Tyrou D., Erraiss N.-E., Vedel M., Touze: Mesnard J., Sautiere P., Wegnez M.;
"Molecular Touring and expression of a metallothionein mRNA in Vences lacking".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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METAL
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PROSITE; PS00203; METALLOTHIONBIN_VRT; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Xenopus laevis metallothionein: mRNA accumulation in response to
NOLX_RHISN P55711;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL;
                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
                                                                       38 CPAECSKC-SQG-CHCEKGSKKCSCCN 62
                                                   31 CASDVSKCLIQELCQCRPGEGNCSCCK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cell Biol. 12:341-349(1993).
FUNCTION: METALLOTHIONEINS HAVE A HIGH CONTENT OF CYSTEINE RESIDUES THAT BIND VARIOUS HEAVY METALS.
DOMAIN: CLASS I METALLOTHIONEINS CONTAIN 2 METAL-BINDING DOMAINS: FOUR DIVALENT IONS ARE CHELATED WITHIN CLUSTER A OF THE ALPHA DOMAIN AND ARE COORDINATED VIA CYSTEINYL THIOLATE BRIDGES TO 11 CYSTEINE LIGANDS. CLUSTER B, THE CORRESPONDING REGION WITHIN THE BETA DOMAIN, CAN LIGATE THREE DIVALENT IONS TO 9 CYSTEINES.
SIMILARITY: BELONGS TO FAMILY 1 IN METALLOTHIONEIN SUPERFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                           U14649; AAB60616.1; ... M96729; AAB59949.1; ... X69380; CAA49177.1; -.. P04355; IMRT.
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                                                                                                                                        62 AA;
                                                                                             Conservative
                                                                                                                                        6403 MW;
                                                                                                                                                             Score 94; DB 1;
Pred. No. 2.54e-01
6; Mismatches
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           596 AA
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Best Local :
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Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1997 (Rel. 35, Cr. 01-NOV-1997 (Rel. 35, La. 01-NOV-1997 (Rel. 35, La. NODULATION PROTEIN NOLX.
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MEDLINE; 89280632.
Olsen D., Nagayoshi T., Fazio M.,
Sanborn D., Sasaki T., Kuivaniemi
                                                                                                                                                                                                                                                                                                                                                                 IMA1_HUMAN STANDARD; PRT; 3075 AA. P25391; P25391; O1-MAY-1992 (Rel. 22, Created) O1-MAY-1992 (Rel. 22, Last sequence update) 15-JUL-1999 (Rel. 38, Last annotation update) 15-JUL-1999 (Rel. 38, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NOLX OR Y4YC.
                                                                                                                                                                                                Haaparanta T., Uitto J., Ruoslahti E., Engvall E.; "Molecular cloning of the cDNA encoding human laminin A chain."; Matrix 11:151-160(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AE000107; AAB91942.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rhizobiaceae; Rhizobium.
                                                                                                                       Nissinen M., Vuolteenaho R., Tryggvason K.;
                                                                                                                                                                                                                                                                                                             Eukaryota;
                                                                                                                                                                                                                                                                                                                                                        LAMININ ALPHA-1 CHAIN PRECURSOR (LAMININ A CHAIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nodulation; Transmembrane; Plasmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE;
                                               SEQUENCE OF 2397-3072 FROM
                                                                              Biochem.
                                                                                                                                                                     SEQUENCE OF 1-2628 FROM N.A.
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                                                                                                                                                                                                                                                                                              Mammalia;
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                                                                                                                                                                                                                                                                                                                                           LAMA1 OR LAMA.
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                                                                                                                                                       MEDLINE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Molecular basis of symbiosis between Rhizobium and legumes.";
                                                                                         Primary structure of the human laminin A chain. Limited expression n human tissues.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            83
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Similarity 29.9%;
23; Conservation
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                                                                                                                                                     91264789.
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                                                                            276:369-379(1991).
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35, Last sequence update)
35, Last annotation update)
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                                               N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 93; DB 1;
Pred. No. 3.58e-01
21; Mismatches 3
                                                                                                                                       Boot-Handford R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL.
04217C948052A733 CRC64;
 Peltonen J., Jaakkola S. H., Chu M.L., Deutzmann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 596;
                                                                                                                                         Kallunki P.,
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LAD. INVEST. 60:772-782(1989).

1- FUNCTION: BINDING TO CELLS VIA A HIGH AFFINITY RECEPTOR, LAMININ IS THOUGHT TO MEDIATE THE ATTACHMENT, MIGRATION, & ORGANIZATION OF CELLS INTO TISSUES DURING EMBRYONIC DEVELOPMENT BY INTERACTING WITH COTHER EXTRACELLULAR MATRIX COMPONENTS.

1- SUBUNIT: LAMININ IS A COMPLEX GLYCOPROTEIN, CONSISTING OF THREE DIFFERENT POLYPEPTIDE CHAINS (ALPHA, BETA, GAMMA), WHICH ARE BOUND TO EACH OTHER BY DISULETIDE BONDS INTO A CROSS-SHAPED MOLECULE COMPRISING ONE LONG & THREE SHORT ARMS WITH GLOBULES AT EACH END. THE ALPHA-1 CHAIN IS A SUBUNIT OF LAMININ-1 (EHS LAMININ) AND LAMININ-3 (S-LAMININ).

1- SUBCELLULAR LOCATION: EXTRACELLULAR.

1- TISSUE SPECIFICITY: FOUND IN THE BASEMENT MEMBRANES (MAJOR COMPONENT).

1- DOMAIN: THE ALPHA-HELICAL DOMAINS I AND II ARE THOUGHT TO INTERACT WITH OTHER LAMININ CHAINS TO FORM A COILED COIL STRUCTURE.

1- SIMILARITY: CONTAINS 1 LAMININ N-TERMINAL DOMAIN (DOMAIN VI).

1- SIMILARITY: CONTAINS 1 LAMININ DOMAINS IV.

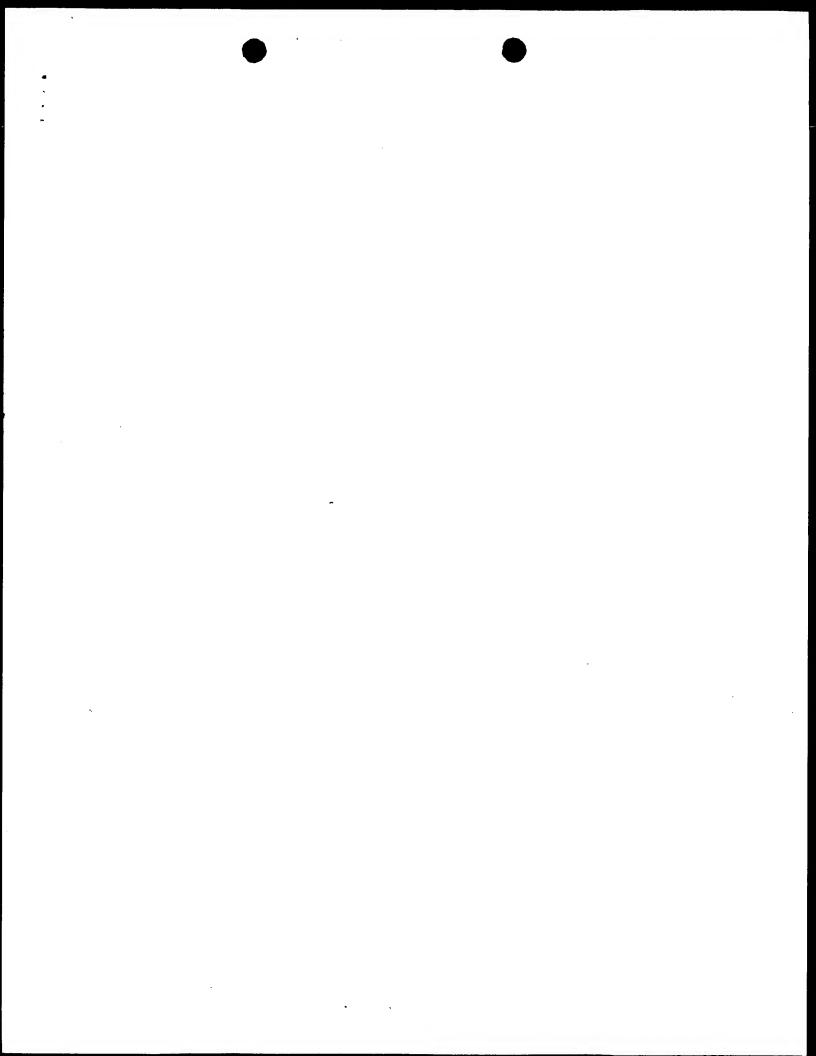
1- SIMILARITY: CONTAINS 5 LAMININ DOMAINS IV.
                                                                                                                                                                                                                                                                                                                                                  Laminin EGF-like domain; C
SIGNAL 1 17
CHAIN 18 3075
DOMAIN 18 269
DOMAIN 270 516
        DOMAIN
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PROSITE; PS00022;
PROSITE; PS01186;
PROSITE; PS01248;
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and B2
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PIR; S14458; S
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PF00054;
PF00055;
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n laminin: cloning and sequence analysis of cDNAs encoding A,
2 chains, and expression of the corresponding genes in human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             S14458.
                                                                                                                                                                                                                                                                                                                                                                                                             Basement membrane; Extracellular matrix; ike domain; Cell adhesion; Repeat; Signal.
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laminin_EGF;
laminin_G; 5.
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EGF_2; 2.
LAMININ_TYPE_EGF; 15.
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LAMININ N-TERMINAL (DO
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IN EGF-LIKE 2.
IN EGF-LIKE 3.
IN EGF-LIKE 4.
IN EGF-LIKE 5 (N-TERMINAL).
IN DOMAIN IV 1 (DOMAIN IV B).
AMININ EGF-LIKE REPEATS (DOMAIN
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N EGF-LIKE 7
N EGF-LIKE 8
N EGF-LIKE 9
N EGF-LIKE 19
N EGF-LIKE 11
        EGF-LIKE
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E 14 (N-TERMINAL).
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Best Local Similarity 35.0%;
Matches 14; Conservative
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Gaps 2;

Search completed: Wed Aug 16 09:32:22 2000 Job time : 42 secs.



(MT)

Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

rch\_pp protein - protein database search, using Smith-Waterman algorithm

Wed Aug 16 09:30:03 2000; MasPar time 13.39 Seconds 785.505 Million cell updates/sec

Tabular output not generated.

Description: Perfect Score:

Sequence: >US-09-416-267-2 (1-223) from US09416267.pep 1738 1 MKLHYVAVLTLAILMFLTWL.....IGPECIDYGSKTVKCMNCMF 223

Scoring table: PAM 150 Gap 11

142080 seqs, 47172406 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

pir64 1:pir1 2:pir2 3:pir3 4:pir4

Statistics: Mean 43.550; Variance 80.722; scale 0.540

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	7			
<ol> <li>Score Match Length DB</li> </ol>				
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esult No.	Score	Query Match	Length	BB	Ü	Description	Pred. No.
<b>L</b>	537	30.9	249	2	A53836	developmental protein	1.06e-87
2	104		798	N	052	-7 cha	.19e-
ω	102		417	N	161	lcal pro	.05e-
4	101	5.8	194	N	S03806		1.11e-01
ъ	100		417	N	T08724		
σ	97		244	N	S71879	4	:_
7	97		806	N	A46271	integrin beta-7 chain	9e-
œ	96		326	N	A38144	adenosine receptor Al	.45e
9	96		446	N	A42108	clusterin precursor -	.45e-
10	95		461	<b>_</b>	A35356	tumor necrosis factor	7.45e-01
11	95		471	N	S35019	nolX protein - Rhizob	.45e
12	96		1801	<b>ب</b>	MMRTS	laminin beta-2 chain	.45e
13	96		3084	مر	MMMSA	laminin alpha-1 chain	.45e
14	94		62	N	I51538	metallothionein - Afr	.01e
15	94		3075	N	S14458	laminin alpha-1 chain	1.01e+00
16	92		130	N	830008	hypothetical protein	1.87e+00
17	92		404	N	A75192		1.87e+00
18	92		627	N	B48442	membrane transport pr	1.87e+00
19	91		53	N	S24596		2.53e+00
20	90		63	N	S08190	metallothionein 1 - p	3.41e+00
21	90		116	N	H72207	dnaJ-related protein	3.41e+00
22	90		157	N	S58018	probable olfactory re	3.41e+00
23	90		167	2	164221	conserved hypothetica	3.41e+00

45	44	43	42	41	40	39	38	37	36	35	34	ယ္	32	31	30	29	28	27	26	25	24
87	87	87	89	89	88	88	88	88	89	89	89	89	88	88	88	90	90	91	91	90	90
5.0	5.0	5.0	5.1	5.1	5.1	5.1	5.1	5.1	5.1	5.1	5.1	5.1	5.1	5.1	5.1				5.2		
565	185	185	3635	1964	1652	1042	757	586	328	326	326	244	140	113	43	925	690	618	445	324	241
N	N	N	N	N	N	N	N	Н	N	N	N	N	N	H	$\vdash$	μ.	N	N	N	N	N
T16408	T15623	148931	T10053	T09059	150711	S43904	T16609	TVVPBP	JN0675	C30341	A53005	JC2425	A48166	S07092	SMFF2	A39216	S54775	S69067	A40018	S55302	T16802
hypothetical protein	hypothetical protein	adenosine receptor su	laminin alpha 5 chain	notch4 - mouse	complement C3 precurs	hyaluronidase - Clost	hypothetical protein	large T antigen - bov	adenosine receptor Al	G protein-coupled rec	adenosine receptor A1	glutathione transfera	gonadotropin II beta	gonadotropin beta cha	metallothionein 2 - f	plasma cell membrane	cell size regulation	probable glycinetRN	clusterin precursor -	A(1) adenosine recept	hypothetical protein
8.24e+00	8.24e+00	8.24e+00	4.59e+00	4.59e+00	6.15e+00	6.15e+00	6.15e+00	6.15e+00	4.59e+00	4.59e+00	4.59e+00	4.59e+00	6.15e+00	6.15e+00	6.15e+00	3.41e+00	3.41e+00	2.53e+00	2.53e+00	3.41e+00	3.41e+00

# ALIGNMENTS

당	Дb	DЪ	Оy	Quer Best Matc	SUMMARY	1-21 22-249	KEYWORDS FEATURE	#gene	GENETICS			5	# 6	#	#title	#au	REFERENCE	DATE	ORGANISM	TITLE	RESULT
164 NKCR	115 IRFS :  : 119 VSFP	58 LNCL :    60 MLCL	1 MKLH 1 H	Query Match Best Local S Matches 7	к	1 249	##Cross- DS E	ne	CS	##residu	##molecule_type	##status	accession	oss-refe	#journal	#authors	NCE		WS		ъ
NKCROQCESMGASSYRWFHDGCCECVGENCLNYGINESRCRGC 206	IRFSMRAGFKQRVQG-GASGDAGNGNGNGNAG-SAGVT-LCTVIYVNSCIRA 163 :   :	LNCLGELYIECCGCLDMC-PKHKDVLPSLTPRSEIGDI-EGVPELFDTLTAEDDE-GWST 114	MOLLCYFVILFVGIAPW-SSLANDDGCNEVVCGSVVSKCLITQSCQCKLNDCHCCKDC 57	Query Match 30.9%; Score 537; DB 2; Length 249; Best Local Similarity 35.4%; Pred. No. 1.06e-87; Matches 79; Conservative 54; Mismatches 71; Indels 19; Gaps 13;	#label MAT #length 249 #molecular-weight 27220 #checksum 1494	<pre>#domain signal sequence #status predicted #label SIG\ #product developmental protein tsq #status predicted</pre>	E mbryo; extracellular protein; glycoprotein	tsg		##residues 1-249 ##Label MAS ##residues 1-249 ##Label MAS	le_type DNA		A53836	<pre>gastrulation, a gene encoding a secreted protein related to human connective tissue growth factor.</pre>		Mason, E.D.; Konrad, K.D.; Webb, C.D.; Marsh, J.L.	A33836	07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change	melanogaster) #formal_name Drosophila melanogaster	developmental protein TSG precursor - fruit fly (Drosophila	

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                                                                                                                          Watson, J.D.; Krissansen, G.W.

#journal Int. Immunol. (1992) 4:1031-1040

#title The gene organization of the human beta 7 subunit,
beta subunit of the leukocyte integrins HML-1 an

#cross-references MUID:93002753
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#title
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#accession A43979
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##molecule_type DNA
##residues 1-798 ##label RE2
##cross-references GB:S49378; NID:g257583; PIDN:AAB23688.1; PID:g257584
                                                                                     ##status
                                                                                                                                                                                                                                                                               ##cross-references GB:S80335; NID:g244680; PIDN:AAB21332.1; PID:g244681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ##molecule_type mRNA
##residues 1-133,'R',135-161,'S',163-309,'S',311-490,'A',493-505,
'A',507-571,'M',573-707,'A',709-730,'W',732-798
##label_YUA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ##molecule_type mRNA
                                                                                                                                                                                                                Jiang, W.M.; Jenkins, D.; Yuan, Q.; Leung, E.; Choo, K.H.;
Watson, J.D.; Krissansen, G.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Cloning and sequence analysis of a novel beta 2-related integrin transcript from T lymphocytes: homology of integrin cysteine-rich repeats to domain III of laminin
                                                                                                          I54749
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Micklem, K.J.; Dong, Y.; Willis, A.; Pulford, K.A.; Visser, L.; Durkop, H.; Poppema, S.; Stein, H.; Mason, D.Y. Am. J. Pathol. (1991) 139:1297-1301
HML-1 antigen on mucosa-associated T cells, activated cells, and hairy leukemic cells is a new integrin containing the beta 7 subunit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Yuan, Q.; Jiang, W.M.; Krissansen, G.W.; Watson, J.D.
Int. Immunol. (1990) 2:1097-1108
Cloning and sequence analysis of a novel beta-2-related
integrin transcript from T lymphocytes: homology of
integrin cysteine-rich repeats to domain III of laminin B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Yuan, Q.A.; Jiang, W.M.; Krissansen, G.W.; Watson, J.D. Int. Immunol. (1991) 3:1373-1374
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Complete amino acid sequence of an integrin beta subunit (beta-7) identified in leukocytes.
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integrin beta-7 chain precursor - human
#formal_name Homo saptens #common_name man
28-Feb-1992 #sequence_revision 28-Feb-1992 #text_change
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Best Local Similarity 27.5%;
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#introns 1
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#map_position 12q13.13-12q13.13
#introns 67/3; 135/1; 192/1; 272/3; 325/3; 357/3; 387/3; 436/3; 501/2;
#introns 576/1; 649/2; 719/1; 772/3
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                                                                                                                                                                                                      175 CMSIHQCKISCESMGASKYR 194
                                                                                                                                                                                                                                                      331 CVNLIR-QLECSGQVKSDFR 349
                                                                                                                                                                                                                                                                                                      116 W-NIVSFPVAEELSHHENLVSFLETVNQPHHQNVSVPSNNVHAPYSSDKEHMCTVVYFDD 174
                                                                                                                                                                                                                                                                                                                                                            273 WFKIVSFSGVEELSVDEFIVS-TKTLQDEEVAAVLLNMSNCNNANKMEKSGSCSFG-FEE 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ##residues
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ##experimental_source cultivar Columbia
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Local Similarity 31.6%;
es 18; Conservative
103/3; 200/1
F19F24.8
#length 417 #molecular-weight 47606 #checksum 1252
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Brandon, R.C.; Sykes, S.M.; Kaul, S.; Mason, T.M.;
Kerlavage, A.R.; Adams, M.D.; Somerville, C.R.; Venter,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    T01616 #type complete
hypothetical protein F19F24.8 - Arabidopsis thaliana
formal_name Arabidopsis thaliana #common_name mouse-ear
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Pred. No. 8.05e-02
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 417;
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                                       #accession
                                                        the liver and lung of mouse, rat cross-references MUID:96358519
                                                                                                                                                                   #authors
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IFICATION #superfamily cytochrome-c oxidase assembly protein COX11
**References EMBL:X05828; NID:g45468; PIDN:CAA29271.1; PID:g45472
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ##residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ##experimental_source fetal kidney; clone DKFZp566D213
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##molecule_type mRNA
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Local Similarity 28.6%;
les 14; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                      19 WIPESISC-NKALCASDVSKCLIQELCQCRPGEGNC-SCCKECMLCLGA 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23 MGALSWAAVPFYSWFCKVTGFAGTTNVAEAASDTVLDEKIRVRF-D-ANADSNLGWTFRP 80
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EMBO J. (1987) 6:2825-2833
Isolation and analysis of the genes for cytochrome
in Paracoccus denitrificans.
                                                                                       Green, T.

Biochem. J. (1996) 318:297-303

The distribution of Theta-class glutathione S-transferases in
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Wiemann, S.
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21-Apr-1997 *sequence_revision 09-May-1997 *text_change
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   #authors Yuan, Q.; Jiang, W.M.; Leung, E.; Hollander,
J.D.; Krissansen, G.W.
#journal J. Biol. Chem. (1992) 267:7352-7358
#title Molecular cloning of the mouse integrin beta
#cross-references_MUID:92218384
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#title
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PID:e245091; PID:g1340078
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##residues 1-123,125-556,'H',558-806 ##label YUA
##cross-references GB:M68903; NID:g349598; PIDN:AAA02749.1; PID:g349599
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                                                                                              ##residues 1-80,'G',82-537,'C',539-806 ##label GUR ##cross-references GB:S44607; NID:g255138; PIDN:AAB2319 ##experimental_source_spieen
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##residues 1-806 ##label HU1
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                                                                                                                                                                ##molecule_type mRNA
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Similarity 30.0%;
21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A46271 #type complete
Integrin beta 7 chain precursor - mouse
M290 antigen beta chain
#formal_name Mus musculus #common_name house mouse
21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change
20-Aug-1999
                                                                                                                                                                                                                                                                   Gurish, M.F.; Bell, A.F.; Smith, T.J.;
R.K.; Weis, J.H.
J. Immunol. (1992) 149:1964-1972
Expression of murine beta 7, alpha 4, a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hu, M.C.; Crowe, D.T.; Weissman, I.L.; Holzmann, B. Proc. Natl. Acad. Sci. U.S.A. (1992) 89:8254-8258 Cloning and expression of mouse integrin beta p(beta 7 functional role in Peyer's patch-specific lymphocyte
                                                                                                                                                                                                                                                                                                                                                          A46503
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Yuan, Q.; Jian, W.; Hollander, Krissansen, G.W.
                                         PN0017
                                                                                                                                                                                                            B46503
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the authors translated the codon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1-244 ##label MAI
                                                             sequence extracted from NCBI backbone (NCBIN:113091, NCBIP:113092)
                                                                                                                                                                                                                                                                                                                                                                                sequence extracted from NCBI backbone (NCBIN:93455,
NCBIP:93463)
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Pred. No. 3.99e-01
21; Mismatches 2
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                                                                                                                          PIDN:AAB23193.1; PID:g255139
                 Leung,
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                                                                                                                                                                                                                                                                                                                     Ducharme, L.A.; Wāng
安康
                   E.; Watson,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               D.; Watson,
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ACCESSIONS
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Best Local Similarity 31.6%;
Matches 18; Conservative
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#title
                                                                                                                            #cross-references MUID:92201360
                                                                                                                                                                                                                                        #authors
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##experimental_source brain
                  #residues 1-100,'M',102-326 ##label TUC
##cross-references EMBL:X63592
                                      ##residues
                                                          ##molecule_type mRNA
                                                                                     ##status
                                                                                                                                                                                                                                                                                                                ##cross-references GB:M86261; NID:g162597; PIDN:AAA30350.1; PID:g162598
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                                                                                                                                                                                                                                                                                                       ##note
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##residues 20-32 ##label KIL
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                                                                                                                                                                  FEBS Lett. (1992) 297:107-111
Cloning and expression of a b
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                                                                                                       S20390
                                                                                                                                                                                                                             Tucker, A.L.; Linden, J.; Robeva, A.S.; D'Angelo, D.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A38144 #type complete
adenosine receptor A1 - bovine
#formal_name Bos primigenius taurus #common_name cattle
04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change
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#product integrin beta 7 chain (fragment) #status
experimental #label IBC
#length 806 #molecular-weight 87411 #checksum 9972
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cell adhesion; cytoskeleton; duplication; extracellular matrix; glycoprotein; heterodimer; membrane protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kilshaw, P.J.; Murant, S.J.
Eur. J. Immunol. (1990) 20:2201-2207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A60229
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Identity between the novel integrin beta 7 subunit and an antigen found highly expressed on intraepithelial lymphocytes in the small intestine.
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                                                                                 nucleic acid sequence not shown
                                                                                                                                                                                                                                                                                              sequence extracted from NCBI backbone (NCBIN:103815,
                                                                                                                                                                                                                                                                                                                                                                    1-326 ##label OLA
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                                                                                                                                                                                                                                                                               NCBIP:103816)
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Pred. No. 3.99e-01;
12; Mismatches 23
                                                                                                                                                                of a bovine adenosine A(1):receptor
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                                                                                                                   Best
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#title
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   #authors Diemer, V.; Hoyle, M.; Baglioni, C.; Millis, A.J.
#journal J. Biol. Chem. (1992) 267:5257-5264
#title Expression of porcine complement cytolysis inhibitor mRNA in cultured aortic smooth muscle cells. Changes during differentiation in vitro.
#cross-references_MUID:92184774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        #accession
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         #cross-references MUID:97318844
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112 TOLINWITYSEPVAEELSHHENLYSELETVIOPHH 145
                                           223 SREARNIMPEPLETDLNYHDMFQPEFDMIHQAQQ 256
                                                                                                                                                                                                                                                                                                                                                                                                      ##molecule_type protein
##residues 58-66,68-77;229-247;249-251,408-436 ##label OG2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ##residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ##residues 1-446 ##label DIE
##cross-references GB:M84639; NID:g164408; PIDN:AAA31013.1; PID:g164409
##experimental_source aortic smooth muscle cells
##note sequence extracted from NCBI backbone (NCBIN:87354,
                                                                                                                                                                                                                                                                                                                                                                                          ##experimental_source pituitary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ##molecule_type DNA
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                                                                                                              Match 5.5%;
Local Similarity 23.5%;
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Local Similarity 37.1%;
les 13; Conservative
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                                                                                                                                                                                                                                                                                                                                                                       #superfamily clusterin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PC4475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   M.; Sakai, T.; Inoue, K.
Biochem. Biophys. Res. Commun. (1997) 234:712-718
The glycopyroteins that occur in the colloids of senescent porcine pituitary glands are clusterin and glycosylated albumin fragments.
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clusterin precursor - pig
complement cytolysis inhibitor; CP40 protein
#formal_name Sus scrofa domestica #common_name domestic
04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change
                                                                                                                                                                               #length 446 #molecular-weight 51774 #checksum 562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ogawa, S.; Ishibashi, Y.; Sakamoto, Y.; Kitamura, K.; Kubo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                #length 326 #molecular-weight 36579 #checksum 6464
                                                                                           Conservative
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#domain clusterin alpha chain #status predicted #label
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                                                                                                              Score 96; DB 2; 1
Pred. No. 5.45e-01;
                                                                                    19; Mismatches
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Pred. No. 5.45e-01
11; Mismatches
                                                                                                                                  Length 446;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             #authors Dembic, 2.; Loetscher, H.; Gubler, U.; Pan, Y.C.; Lahm, H.W.; Gentz, R.; Brockhaus, M.; Lesslauer, W.
#journal Cytokine (1990) 2:231-237
#title Two human TNF receptors have similar extracellular, but distinct intracellular, domain sequences.
#cross-references_MUID:91370690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                #journal Proc. Natl. Acad. Sci. U.S.A. (1990) 87:6151-6155
#title Complementary DNA cloning of a receptor for tumor necrosis
factor and demonstration of a shed form of the receptor.
#cross-references_MUID:90349572
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# title A receptor for tumor necrosis factor defines an unusual family of cellular and viral proteins.

# cross-references MUID:90260639
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#accession A23666
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##molecule_type mRNA; protein
##residues_4461 ##label DEM
##cross-references GB:563368; NID:g235648; PIDN:AAB19824.1; PID:g235649
##note sequence extracted from NCBI backbone (NCBIN:63368,
NCBIP:63371)
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                                                                 ##residues
                                                                                           ##molecule_type protein
                                                                                                                               ##status
                                                                                                                                                                                                                                                                                                                                                                                                      ##sstatus preliminary
##molecule_type mRNA
##rosidues 116-140,'p',142-195,'R',197-362,'T',364-461 ##label HEL
##cross-references GB:M35857; NID:g339751; PIDN:AAA63262.1; PID:g339752
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A second tumor necrosis factor receptor gene product can shed a naturally occurring tumor necrosis factor inhibitor.
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Lesslauer, W.; Brockhaus, M.
J. Biol. Chem. (1990) 265:20131-20138
Purification and partial amino acid sequence analysis of two distinct tumor necrosis factor receptors from HI60 cells.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             75K tumor necrosis factor receptor #formal_name Homo sapiens #common_name man 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change
A35010 Engelmann, H.; Novick, D.; Wallach, D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Heller, R.A.; Song, K.; Onasch, M.A.; Fischer, W.H.; Chang, D.; Ringold, G.M.
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Best Local Similarity 42.4%;
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78-119
120-162
164-201
262-279
280-461
171,193
                                                                                         #authors Meinhardt, L.W.; Krishnan, H.B.; Balatti, P.A.; Pueppke, S.G.
#journal Mol. Microbiol. (1993) 9:17-29
#title Molecular cloning and characterization of a sym plasmid locus
that regulates cultivar-specific nodulation of soybean by
Rhizobium fredii USDA257.
#cross-references MUID:94018604
#accession S35019
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23-416
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#journal Gene (1994) 150:381-386
#title Cloning, sequencing and partial functional characterization
#title of the 5' region of the human p75 tumor necrosis factor
receptor-encoding gene (TNF-R).
#cross-references_MUID:95121934
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#title
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##molecule_type protein
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p_position 1p36.2-1p36.2
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#formal_name Rhizobium fredii
03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change
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receptor repeat homology
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#domain NGF receptor repeat homology #label NG1\
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#domain NGF receptor repeat homology #label NG3\
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#product tumor necrosis factor receptor type 2 #status
                                                  1-471 ##label MEI
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the authors translated the codon GAA for residue 309
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1 461 #mo
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CLASSIFICATION
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880-927
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286-555
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                                                                                                                                                                           989-1038
                                                                                                                                                                                                    930-986
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251,371,1088,1252,
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                                             .446-1801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ##residues 1-1801 ##label HUN
##cross-references EMBL:X16563; NID:g57250; PIDN:CAA34561.1; PID:g57251
X Laminins are trimers of an alpha-type, a beta-type, and a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                156 PSTPPDLKAAIEALLQD-PELFYAIGSQGDGRCGGKITAKDLSEFSKHHPQVAAFQESQA 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ##molecule_type mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       142 QPHHQNVSVPSNNVHAP 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              215 QSYAQNY-IPSDSAENA 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 29.9%; les 23; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       83 SDTPPTSKSTVEELHEPIPSLFRAL-TEGDTQLNWNIVSFPVAEELSHHENLVSFLETVN 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MMRTS #type complete
laminin beta-2 chain precursor - rat
laminin chain B3; S-laminin
#formal_name Rattus norvegicus #common_name Norway rat
30.-Jun-1991 #sequence_revision 30.-Jun-1991 #text_change
16-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                interact with cells and with other basement membrane proteins to promote differentiation, development, and cell migration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hunter, D.D.; Shah, V.; Merlie, J.P.; Sanes, J.R. Nature (1989) 338:229-234
A laminin-like adhesive protein concentrated in the cleft of the neuromuscular junction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                S03539
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sement membrane; calcium binding; cell binding; coiled coil; extracellular matrix; glycoprotein; heptad repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gamma-type laminin chain.
             #domain I, heptao
#disulfide_bonds
                                             #domain alpha #label ALP\
#domain I, heptad repeats
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                                                                                                  tin laminin type EGF-like homology #label LEO6\
tin III #label DOM3\
tin laminin-type EGF-like homology #label LEO7\
tin laminin-type EGF-like homology #label LEO9\
tin laminin-type EGF-like homology #label LEO9\
tin laminin-type EGF-like homology #label LEI0\
tin laminin-type EGF-like homology #label LEI1\
tin laminin-type EGF-like homology #label LEI1\
tin laminin-type EGF-like homology #label LEI2\
tin laminin-type EGF-like homology #label LEI2\
tin laminin-type EGF-like homology #label LEI2\
tin laminin-type EGF-like homology #label LEI3\
tin laminin-type EGF-like homology #label LEI3\
tin laminin-type EGF-like homology #label LEI3\
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                                         heptad repeats #label DOMI\
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Pred. No. 7.45e-01;
21; Mismatches 30;
                                                                                    heptad
                  #status predicted\
                                                                                    repeats #label DOM2\
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                                                                                                                                                                                                                                                                                                                                                homology #status atypical
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#title
                                                ligand-binding assays.
#cross-references MUID:89078415
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#title Laminin, a multidomain protein. The A chain has a unique
globular domain and homology with the basement membrane
proteoglycan and the laminin B chains.

#cross-references MUID:89034134

#accession A31771
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                                                                                                                                                                                                                                                                                                             ##nolecule_type protein
##residues 311-335,'N',337-339;630-642,'D',644;692-734;737-748,'X',
750-760,'G',762-763;765-769,'X',771,'H',773-778;
780-786,'X',788-802;'Q',839-852,'Q',854-855,'QXQ',
859-869,'Q',871-874;1148-1158;1353-1389;1449-1459
##label HA2 7 is inconsistent with that from
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ##molecule_type mRNA
##residues 1-208,'T',210-334 ##label HAR
##cross-references EMBL:X07737; NID:g52857; PIDN:CAA30561.1; PID:g52858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ##molecule_type protein

183-195,570-571,'A',573-586,596-612,'X',614-617,'EMK';

##residues 183-195,570-571,'A',573-586,596-612,'X',614-617,'EMK';

303-646;1217-1222,'YEF',1226-1227;1303-1310;1498-1507;

2033-2040,'X',2042-2043;2137-2151;2156-2178;2227-2240;

2406-2420;2440-2451;2481-2486,2624-2639;2818-2843;
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##residues 1-3084 ##label SAS
##molecule_type protein
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Local Similarity 36.7%;
nes 11; Conservative
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                                                                                            Mann, K.; Deutzmann, R.; Timpl, R.
Eur. J. Biochem. (1988) 178:71-80
Characterization of proteolytic fragments of the
laminin-nidogen complex and their activity in
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                             S08895
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Eur. J. Biochem. (1988) 173:629-635
The N terminus of laminin A chain is homologous to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       S00624
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laminin chain Al
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          chains.
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                                                                                                                                                                                                                                 the sequence from Fig. 7 is inconsistent with that from Fig. 5 in having 209-11e, 239-Thr, and 240-Arg; the sequence from Fig. 7 is inconsistent with that from Table 1 in having 335-Thr
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#disulfide_bonds interchain #status predicted
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                                                                                                                                                                                                                                                                FEATURE
                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION
        277-331
278-519
334-401
404-458
461-507
510-519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human laminin: cloning and sequence analysis of cDNAs encoding A, B1 and B2 chains, and expression of the corresponding genes in human skin and cultured cells. #access wuld:89280632
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#title Structural study of long arm fragments of laminin. Evidence for repetitive C-terminal sequences in the A-chain, not present in the B-chains.

#cross_references_MUID:89030693
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##molecule_type protein

1911-1929;1997-2006;2033-2045,'X',2047-2054,'X',

2056-2066,'X',2066-2105;2120-2170;2182-2192,'TR';

2209-2216;2227-2240;2247-2251,'X',2253-2266;2289-2298;

2406-2420;2424-2435;2440-2451;2461-2470;2487-2498;

2502-2555;2558-2557;2561-2591,'X',2593-2594;2600-2610;

2616-2645;26468-2655;2650-2722;2754-2780;2795-2805;

2811-2816;2818-2834;2836-2843;2858-2875,'D',2877-2913;

2935-2964;2969-2976;2980-2993;2998-3005,'A',3007-3033,

'Y',3035;3068-3083-#Habel DE2
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2424-2446;2440-2451;2461-2467;2487-2555;2550-2557;

2561-2593;2600-2610;2616-2645;2648-2655;2690-2704;

2707-2722;2754,'L',2756-2780;2795-2805;2811-2816;

2818-2844;2858-2904,'D',2906-2913;2935-2942,'T',

2944-2964;2869-2976;2980-2993;2998-3000,'I',3002-3018,

'V',3020-3034;3068-3083 ##label OLS

Laminins are trimers of an alpha-type, a beta-type, and a

gamma-type laminin chain.
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##residues 630-642,'D',644;2690-2704 ##label FUJ
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                                                                                                                                                                                                                                                                           interact with cells and with other basement membrane proteins to promote differentiation, development, and cell migration #superfamily laminin alpha-1 chain; laminin G repeat homology; laminin-type EGF-11ke homology basement membrane; calcium binding; cell binding; coiled coil; extracellular matrix; glycoprotein; heparin binding; heptad repeat; heterotrimer; pyroglutamic acid
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Biochem. J. (1988) 252:453-461
Structure and distribution of N-linked oligosaccharide chains on various domains of mouse tumour laminin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Olsen, D.; Nagayoshi, T.; Fazio, M.; Peltonen, J.; Jaakkola, S.; Sanborn, D.; Sasaki, T.; Kuivaniemi, H.; Chu, M.L.; Deutzmann, R.; Timpl, R.; Uitto, J. Lab. Invest. (1989) 60:772-782

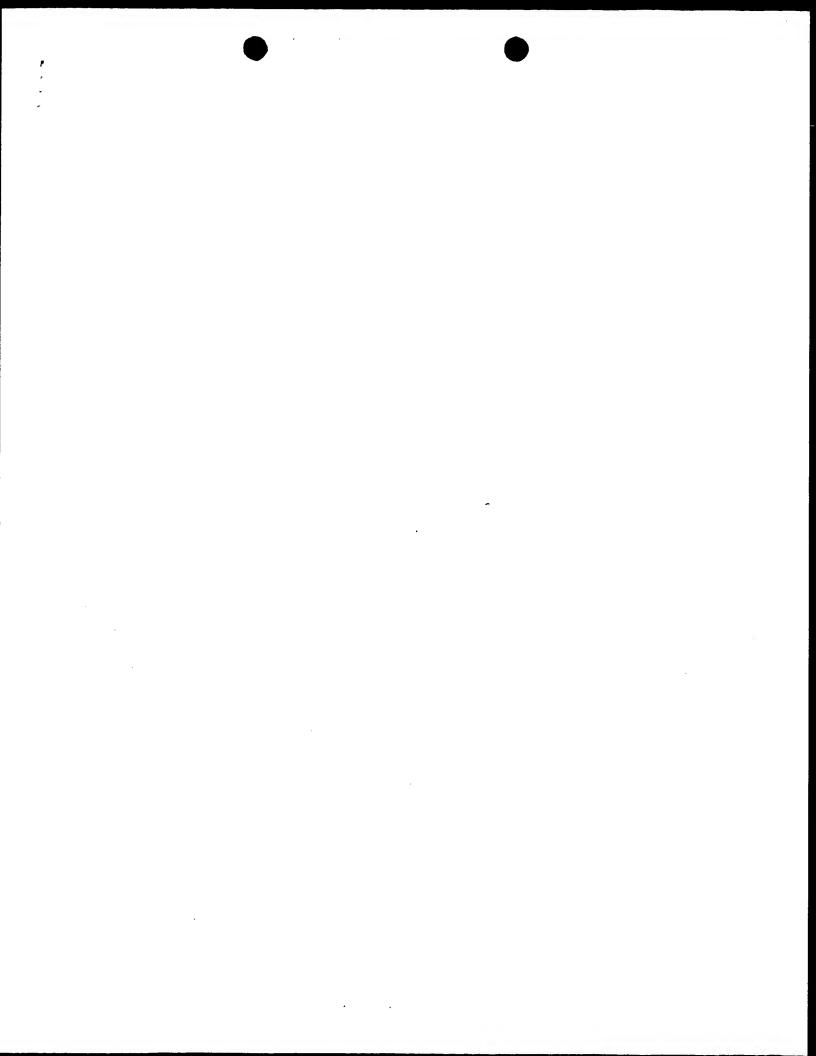
Human laminin: cloning and sequence analysis of cDNAs
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Olsen,
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S02678
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#domain V #label DOM5\
                                                                                                                                                           #domain VI #label DOM6\
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#product laminin alpha-1 chain #status predicted #label
laminin-type EGF-like
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homology #label LE02\homology #label LE03\homology #label LE04\homology #status atyp
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798-853
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716-1166
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2150-2308
2337-2492
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770,857,1999,2055,
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562,672,808,914,
959,969,1052,1344,
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1718,1725,1763,
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1936,1982,1993,
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Local Similarity 37.5%;
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                                        netallothionein - African clawed frog
metallothionein - African clawed frog
#formal_name Xenopus laevis #common_name African clawed
13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change
20-Aug-1999
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#domain laminin-type EGF-like homology #label LE19\
#domain laminin-type EGF-like homology #label LE20\
#domain laminin-type EGF-like homology #label LE20\
#domain laminin-type EGF-like homology #label LE20\
#domain laminin G repeat homology #label LG1\
#domain laminin G repeat homology #label LG3\
#domain laminin G repeat homology #label LG5\
#modified_site pyrrolidone carboxylic acid (Gln) (in mature form) #status predicted\
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#domain IIIb #label DO3B\
#domain laminin-type EGF-like homology #status atypical
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#label LE15\
#region cell attachment (R-G-D) motif\
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#domain laminin-type EGF-like
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homology #status atypical
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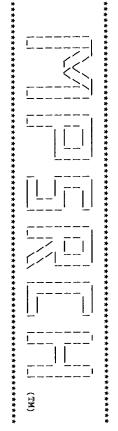
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##cross-references GDB:120135; OMIM:150320
#map_position 18p11.32-18p11.22
CLASSIFICATION #superfamily laminin alpha-1 chain; laminin
                                                                                                                      GENETICS
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#cross-references MUID:89280632
#accession A34961
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#journal
#title
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#journal Biochem. J. (1991) 276:369-379
#title Primary structure of the human laminin A chain. Limited expression in human tissues.
#cross-references_MUID:91264789
                                                                                          #gene
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#journal Matrix (1991) 11:151-160
#title Molecular cloring of the cDNA encoding human laminin A chain.
#cross-references MUID:91333420
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Local Similarity 44.4%;
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DNA Cell Biol. (1993) 12:329-340
Cloning and nucleotide sequence of a complementary DNA
encoding Xenopus laevis metallothionein: mRNA accumulation
in response to heavy metals.
TELECOMINION OF THE PROPERTY OF 
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30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change
13-Aug-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Olsen, D.; Nagayoshi, T.; Fazio, M.; Peltonen, J.; Jaakkola, S.; Sanborn, D.; Sasaki, T.; Kuivaniemi, H.; Chu, M.L.; Deutzmann, R.; Timpl, R.; Uitto, J.
Lab. Invest. (1989) 60:772-782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        S14663
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#length 62 #molecular-weight 6403 #checksum 3001
                                                                                          GDB:LAMA1; LAMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     S14458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      S14458; S14663; A34961
S14458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     not compared with conceptual translation
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                                                                                                                                                                      the authors translated the codon AGA for residue 2692 as
                                                                                                                                                                                                                                                                                 not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                           W', 2397-2745, 'L', 2747-3053, 'L', 3055-3072, 'PSP' ##label
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        G repeat
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                                                                                                                                               Matches
                                                                                                                                                                      Query Match
Best Local.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         801,838,926,952,
1045,1407,1579,
1596,1678,1689,
1698,1717,1804,
1894,1898,1957,
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709-1159
709-739
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270-516
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1452-1506
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1362-1553
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791-846
849-899
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                                                                                 1084 FPDCVPCDCDLRGTSGDACNLEQGLCGCVEETGACPC-KE 1122
                                                                                                                                                                   Match 5.4%;
Local Similarity 35.0%;
                                    20 LPESLSCNKALCASDVSKC-LIQELCQCRPGEGNCSCCKE 58
                                                                                                                                                                                                                                                  #disulfide_bonds #status predicted
#length 3075 #molecular-weight 337155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            homology, laminin-type EGF-like homology basement membrane; calcium binding; cell binding; coiled coil; disulfide bond; extracellular matrix; glycoprotein; heparin binding; heptad repeat; heterotrimer
                                                                                                                                          Conservative
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#domain laminin G repeat homology *label LG2\
#domain laminin G repeat homology *label LG3\
#domain laminin G repeat homology *label LG3\
#region cell attachment (R-G-D) motif\
#domain laminin G repeat homology *label LG4\
#domain laminin G repeat homology *label LG5\
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              #domain laminin-type EGF-11ke homology #label
#domain laminin-type EGF-11ke homology #label
#domain I/II, heptad repeats #label DOM2\
#region cell attachment #status predicted\
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#domain laminin-type EGF-like homology #label LE19\
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#label LE16\
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#label LE15\
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#domain laminin-type EGF-like
#domain laminin-type EGF-like
#domain laminin-type EGF-like
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#product laminin alpha-1 chain #status predicted #label
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                                                                                                                                                                   Score 94; DB 2;
Pred. No. 1.01e+00
                                                                                                                                          89
                                                                                                                                          Mismatches
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                                                                                                                                          16;
                                                                                                                                                                                            Length 3075;
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/ #label LE2\
/ #label LE3\
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LE8/
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LE11\
LE12\
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2;

ENTRY TITLE

Search completed: Wed Aug 16 09:31:22 2000 Job time : 79 secs.





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Run on: srch\_pp protein - protein database search, using Smith-Waterman algorithm Wed Aug 16 09:35:45 2000; MasPar time 32.75 Seconds 685.348 Million cell updates/sec

Tabular output not generated.

Title:

Description: Perfect Score: >US-09-416-267-2 (1-223) from US09416267.pep 1738

Sequence: 1 MKLHYVAVLTLAILMFLTWL.....IGPECIDYGSKTVKCMNCMF 223

Scoring table: PAM 150 Gap 11

Searched: 709830 seqs, 100662141 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

a-pending
1:PCT 2:U6 3:U60 4:U7 5:U80 6:U81 7:U82 8:U83 9:U84A
1:DCT 2:U6 3:U80 13:U87 14:U88 15:U89 16:U90 17:U91
10:U948 11:U85 12:U86 13:U87 14:U88 15:U89 16:U90 17:U91
18:U92 19:U93 20:U94 21:U95 22:NEWP 23:NEWU60 24:NEWU7
25:NEWU8 26:NEWU9

Statistics: Mean 35.638; Variance 129.125; scale 0.276

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	Result No.
1738 1738 1738 1738 1738 1738 838 838 761 761 761 761 761 761 761 761 761 761	Score
100.0 100.0	Query Match L
223 14 223 14 223 14 223 14 223 15 113 15 1128 23 1128 23 1128 23 206 24 206 24 207 24 208 24 209 24 21 21 22 21 24 22 34 24 34 24 24 24 24 24 24 24 24 24 24 24 24 24	Length DB
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US-09-416- PCT-US98-0 US-08-829-0 PCT-US96-0 US-08-843- US-09-330- US-60-169- US-60-1197- US-60-147- US-09-307- US-09-307- US-09-307- US-09-4167- US-09-1157- US-09-270- US-09-270-	ID
Sequence	Description
2, Applicatio 2, Applicatio 2, Applicatio 2, Applicatio 2, Applicatio 7, Applicatio 7, Applicat 463, Applicat 463, Applicat 463, Applicat 46440, Applicat 14313, Applicat 1946, Applicat 9, Applicatio 9, Applicatio 10403, Applicatio 112, Applicatio	On .
6.64e-185 6.64e-185 6.64e-185 6.64e-185 6.64e-185 6.64e-185 6.91e-71 5.91e-71 5.91e-71 5.91e-71 5.91e-71 5.91e-71 5.91e-71 5.91e-71 5.91e-71 5.91e-71 6.31e-46 5.34e-46 5.34e-46 5.34e-46 5.34e-46 5.34e-46 5.34e-46 5.34e-46	Pred. No.

8888888888888888888888888888888888888	XEX	g X A		
H GBO	Sequ	XXXXXX	-Sn LTD	22222222222222222222222222222222222222
Sequence 2, AJ GENERAL INFO. APPLICANT: APPLICANT: TITLE OF TORRESPOND ADDRESSE STREET: COUNTRY: COUNT	equence 2	×	1 09-416-	1111112 1111100 11100000 11000000 11000000 11000000
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FORMATION:  FORMATION:  TI: LI, YI  TI: SU, KUI  TI: SEE: Human Genon  SEE: IBM PC COMPE  TYPE: Floppy di  TYPE: TOMP  TO	ication		STA	116 798 798 420 420 420 434 434 434 434 434 434 434 430 580 880 898 1345 11801
POM	SD		STANDARD;	115 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
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CCYTOKINE Sciences, enue ble ble jMS-DOS iSe #1.0, 19/416,267 PF270P1 ON:	67		PRT;	
POLYPEPTIDE , Version #1. 57			223 AA	sequence
TIDE #1.3			r	
ő				19960, Applicati 14, Applicati 5942, Applicati 5, Applicati 16, Applicati 16, Applicat 114, Applicat 138, Applicat 13709, Applicat 13707, Applicat 13707, Applicat 130, Applicat 130, Applicati 2, Applicati 2, Applicati 2, Applicati 2, Applicati 3, Applicati 2, Applicati 3, Applicati 3, Applicati 2, Applicati 3, Applicati 3, Applicati 4, Applicati 5, Applicati 6, Applicati 6, Applicati 7, Applicati 8, Applicati 9, Applicati 16, Applicati 17, Applicati 18, Applicati 19, Applicati 10, Applicati 10, Applicati
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       US-08-820-970-2
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                                                                                      181 CKISCESMGASKYRWFHNACCECIGPECIDYGSKTVKCMNCMF 223
                                                                                                                                   121 FPVAEELSHHENLVSFLETVNQPHHQNVSVPSNNVHAPYSSDKEHMCTVVYFDDCMSIHQ 180
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                                                            181 CKISCESMGASKYRWFHNACCECIGPECIDYGSKTVKCMNCMF
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COURENT FILING DATE: 1998-04-15
EARLIER APPLICATION NUMBER: US 08/843,651
EARLIER FILING DATE: 1997-04-16
NUMBER OF SEQ ID NOS: 2
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Homo sapiens
ORGANISM: 4000 sapiens
ORGANISM: 223 AA; 25017 MW; 262453 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Millennium Biotherapeutics, Inc.
TITLE OF INVENTION: NOVEL PEPTIDES WITHIN THE GROWTH FACTOR SUPERFAMILY
FILE REFERENCE: 09404/027W01
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Local Similarity 100.0%;
hes 223; Conservative
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ENCE 223 AA;
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Similarity 100.0%;
   STANDARD;
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25017 MW; 262453 CN;
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Pred. No. 6.64e-185;
0; Mismatches 0;
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Pred. No. 6.64e-185;
0; Mismatches 0;
    223 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 301-309-531.
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
SEQUENCE 223 amino acids
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                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: BIOOKES, Anders, A.
REGISTRATION UMBER: 36,373
REFERENCE/DOCKET NUMBER: PF27
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-309-8504
                                                                                                                                                                                                                                                                                                                                                                                    Local
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/820,970
FILING DATE: 20-MAR-1997
CLASSIFICATION: 435
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein
JENCE 223 AA; 25017 MW; 262453 CN;
                                                                                                                      CKISCESMGASKYRWFHNACCECIGPECIDYGSKTVKCMNCMF 223
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                FPVAEELSHHENLVSFLETVNQPHHQNVSVPSNNVHAPYSSDKEHMCTVVYFDDCMSIHQ
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CITY: ROCKVILLE
STATE: MARYLAND
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APPLICANT: SU, KUI
APPLICANT: LI, HAODONG
TITLE OF INVENTION: HU
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l Similarity 100.0%;
223; Conservative
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                                                                   STANDARD;
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Pred. No. 6.64e-185;
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                                                              Sequence 2, Application US/08843651
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                Sequence 2, Application US/08843651 GENERAL INFORMATION:
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Local Similarity 100.0%;
hes 223; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
NAME: FEITATO, Gregory D
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 3258
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201,994-1700
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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CORRESPONDENCE ADDRESS:
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APPLICANT: SU, KUI
 APPLICANT:
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CITY: RC
STATE: N
COUNTRY:
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 Holtzman, Douglas
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                                                                                                                                                           STANDARD;
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Pred. No. 6.64e-185;
0; Mismatches 0;
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FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Meiklejohn, Ph.D., Anita L.
NAME: Meiklejohn, Ph.D., Anita L.
REGISTRATION NUMBER: 35,283
REFERENCE/DOCKET NUMBER: 09404/027(
TELECOMMUNICATION INFORMATION:
TOTEPHONE: 617/542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                             Sequence 7, Application US/09015412
                                                                                                                                                           XXXXXX
                                                                                                                                                                                          US-09-015-412-7
Sequence 7, Application US/09015412 GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L. APPLICANT: Lal, Preeti
APPLICANT: Corley, Neil C.
                                                                                                                                                                                                                                                     181 CKISCESMGASKYRWFHNACCECIGPECIDYGSKTVKCMNCMF
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                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MKLHYVAVLTLAILMFLTWLPESLSCNKALCASDVSKCLIQELCQCRPGEGNCSCCKECM
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OPERATING SYSTEM: Windows95
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/843,651
FILING DATE: 16-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein FRAGMENT TYPE: interna
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TELEFAX: O1.,
                                                                                                                                                                                                                                                                                                                   FPVAEELSHHENLVSFLETVNQPHHQNVSVPSNNVHAPYSSDKEHMCTVVYFDDCMSIHQ
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Similarity 100.0%;
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Pred. No. 6.64e-185;
0; Mismatches 0;
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Best Local s
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          Sequence 437,
                                                       XXXXXX
                                                                           US-09-330-781-437
                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                181 CKISCESMGASKYRWFHNACCECIGPECIDYGSKTVKCMNCMF 223
                                                                                                                                                                         121 FPVAEELSHHENLVSFLETVNQPHHQNVSVPSNNVHAPYSSDKEHMCTVVYFDDCMSIHQ 180
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                                                                                                                                                                                                                   61 LCLGALWDECCDCVGMCNPRNYSDTPPTSKSTYEELHEPIPSLFRALTEGDTQLNWNIVS 120
                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: PETELECOMMUNICATION INFORMATION: TELEPHONE: 650-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: FastSEQ for CURRENT APPLICATION DATA:
                                                                                                                      CKISCESMGASKYRWFHNACCECIGPECIDYGSKTVKCMNCMF 223
                                                                                                                                                             FPVAEELSHHENLVSFLETVNQPHHQNVSVPSNNVHAPYSSDKEHMCTVVYFDDCMSIHQ
                                                                                                                                                                                                         LCLGALWDECCDCVGMCNPRNYSDTPPTSKSTVEELHEPIPSLFRALTEGDTQLNWNIVS 120
                                                                                                                                                                                                                                                                                                                                                                           IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: PRIOR APPLICATION DATA:
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MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Baugh, Mariah
APPLICANT: Guegler, Karl J.
APPLICANT: Tang, Y. Tom
TITLE OF INVENTION: HUMAN GROWTH FACTOR HOMOLOGS
NUMBER OF SEQUENCES: 12
                                                                                                                                                                                                                                                                                                                                                      LIBRARY: BRONNOT01
CLONE: 3577857
                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Billings, Lucy J. REGISTRATION NUMBER: 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: FILING DATE: Filed
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Similarity 100.0%;
223; Conservative
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          Application US/09330781
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FastSEQ for Windows Version
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                                                                           STANDARD;
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                                                                                                                                                                                                                                                                                                       Score 1738; DB 16; Pred. No. 6.64e-185;
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            Query Match 43.88;
Best Local Similarity 93.88;
   Matches
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                                                                                                         NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patent.pm
SEQ ID NO 463
LENGTH: 125
TYPE: PRT
                                                   SEQUENCE
                                                                                                                                                                                                                                                                                      Sequence 463, Application US/60169629
                                                                                                                                                                                                                                                                                                                                       XXXXXX
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EARLIER FILING DATE: 1998-06-22
NUMBER OF SEQ ID NOS: 490
SOFTWARE: FastsEQ for Windows Version 3
SEQ ID NO 437
LENGTH: 113
                                                                                                                                                                                                                                                     Sequence 463, Application US/60169629 GENERAL INFORMATION:
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GENERAL INFORMATION:
APPLICANT: Gearing, David P.
APPLICANT: Robison, Keith E.
APPLICANT: Holtzman, Douglas A.
APPLICANT: Holtzman, Douglas A.
TITLE OF INVENTION: Nucleic Acid Molecules
TITLE OF INVENTION: Human prostate Stromal
FILE REFERENCE: MLN98-26pA
                                                                                                                                                                  TITLE OF INVENTION: CDNAS for Secreted Proteins FILE REFERENCE: GENSET.071PF CURRENT APPLICATION NUMBER: US/60/169,629 CURRENT FILING DATE: 1999-12-08
                                                                                                                                                                                                               APPLICANT: Dumas Milne Edwards, J.B. APPLICANT: Bougueleret, L. APPLICANT: Jobert, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:

NAME/KEY: SIGNAL

LOCATION: (1)...(25)

NAME/KEY: VARIANT

LOCATION: (1)...(113)

OTHER INFORMATION: Xea = An

EQUENCE 113 AA; 12537 MW; 6
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CURRENT FILING DATE: 1999-06-11
                                              NAME/KEY: SIGNAL
LOCATION: -14..-1
QUENCE: 125 AA; 13870 MW; 87972 CN;
                                                                                   ORGANISM: Homo sapiens FEATURE:
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Similarity 98.18;
   Conservative
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           Score 761; DB 3;
Pred. No. 5.91e-71
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Pred. No. 8.13e-80;
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 Mismatches
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                      Length 125
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Indels 1;
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APPLICANT: Dumas milne Edwar
APPLICANT: Bougueleret, L.
APPLICANT: Jobert, S.
TITLE OF INVENTION: CDNAS fc
FILE REFERENCE: 78.US2.PRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 463, Application US/60187470
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SOFTWARE: Patent.pm
SEQ ID NO 463
LENGTH: 125
TYPE: PRT
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CURRENT APPLICATION NUMBER: US/60/197,873
CURRENT FILING DATE: 2000-04-18
NUMBER OF SEQ ID NOS: 52153
SOFTWARE: Patent.pm
SEQ ID NO 14313
                                                                                                                                                                                                                                                                                                                                                         Sequence 14313, Application US/60197873 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           120 SFPVAEELSHHENLVSFLETVNQPHHQNVSVPSNNVHAPYSSDKEHMCTVVYF 172
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|||||||||||| : | : |
|20 SFPVAEELSHHENLVSFLETVNQPHHQNVSVPSNNVHAPYSSDKEHMCTVVYF 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            60
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Local Similarity 93.8%;
                                                                                                                                            APPLICANT: Giordano, Jean-Yves
TITLE OF INVENTION: ESTs and Encoded Human Proteins
FILE REFERENCE: 81.US1.PRO
                                                                                                                                                                                                                                  APPLICANT: Bejanin, Stephane
APPLICANT: Tanaka, Hiroaki
APPLICANT: Dumas Milne Edwards, Jean Baptiste
APPLICANT: Jobert, Severin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/60/187,470 CURRENT FILING DATE: 2000-03-06
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Pred. No. 5.91e-71;
2; Mismatches 4
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Best Local :
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Best Local (
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APPLICANT: Jobert, S.
APPLICANT: Glordano, J.Y.
APPLICANT: Glordano, J.Y.
TITLE OF INVENTION: ESTS and Encoded Human Proteins.
FILE REFERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/60/147,499
CURRENT FILING DATE: 1999-08-05
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 4240
LENGTH: 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
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                                                                                                                                                                                                                                                                                                  SEQUENCE
                      Sequence 1146, Application US/09307140
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                                                                                                US-09-307-140-1146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 4240, Application US/60147499
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Local Similarity 93.8%;
                                                                                                                                                                                                 60 MLCLGALWDECCDCVGMCNPRNYSDTPPTSKSTVEELHEPIPSLFRALTEGDTQLNWNIV 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  60 MLCLGALWDECCDCVGMCNPRNYSDTPPTSKSTVEELHEPIPSLFRALTEGDTQLNWNIV
                                                                                                                                                                        61 SFPVAEELSHHENLVSFLETVNQPHHQNVSVPSNNVHAPYSSDKGN-CQQLTF 112
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LOCATION: -14..-1
QUENCE 128 AA; 14367 MW; 96202 CN;
                                                                                                                                                                                                                          1 MLCLGALWDECCDCVGMCNPRNYSDTPPTSKSTVEELHEPIPSLFRALTEGDTQLNWNIV 60
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TYPE: PRT
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                                                                                                                                                                                                                                                                                                                           FEATURE:
NAME/KEY: SIGNAL
                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
                                                                                                                                                                                                                                                                                                                 LOCATION: -14..-1
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                                                                                                                                                 SFPVAEELSHHENLVSFLETVNQPHHQNVSVPSNNVHAPYSSDKEHMCTVVYF 172
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                                                                                                                                                                                                                                                             similarity 93.8%;
                                                                                                                                                                                                                                                                                                  128 AA; 14367 MW; 96202 CN;
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                                                                                                STANDARD;
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Pred. No. 5.91e-71;
2; Mismatches 4
                                                                                                                                                                                                                                                  Score 761; DB 3;
Pred. No. 5.91e-71;
2; Mismatches 4
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Sequence 1146, Application US/09307140

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CURRENT APPLICATION NUMBER: US/09/307,140
CURRENT FILING DATE: 1999-05-07
EARLIER APPLICATION UNMBER: 60/084,565
EARLIER FILING DATE: 1998-05-07
NUMBER OF SEQ ID NOS: 1168
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1146
LENGTH: 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 9, Application US/08820970
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APPLICANT: Gearing, David P.
APPLICANT: Holizman, Douglas A.
APPLICANT: Robison, Keith E.
TITLE OF INVENTION: Nucleic Acid Molecules Derived from a
TITLE OF INVENTION: Human Aortic Endothelium Library
FILE REFERENCE: MLN98-14pA
   ATTORNEY_AGENT INFORMATION:

NAME: Brookes, Anders, A.

REGISTRATION NUMBER: 36,373

REFERENCE/DOCKET NUMBER: PE27

TELECOMMUNICATION INFORMATION:

TELEPHONE: 301-309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Match 35.2%;
Local Similarity 100.0%;
les 74; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: SIGNAL
LOCATION: (1)...(25)
QUENCE 75 AA; 8284 MW; 24423 CN;
                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                            APPLICANT: SU, KUI
APPLICANT: LI, HAODONG
TITLE OF INVENTION: HUMAN CYTOKINE POLYPEPTIDE
NUMBER OF SEQUENCES: 9
                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                              STREET: 9410 KEY
CITY: ROCKVILLE
STATE: MARYLAND
COUNTRY: USA
ZIP: 20850
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MKLHYVAVLTLAILMFLTWLPESLSCNKALCASDVSKCLIQELCQCRPGEGNCSCCKECM 60
                                                                                              APPLICATION NUMBER: US/0
FILING DATE: 20-MAR-1997
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                               ADDRESSEE:
                                                                                                                                                                                                                                                                                                                E: HUMAN GENOME SCIENCES, INC
9410 KEY WEST AVENUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                 US/08/820,970
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 9, Application PC/TUS9603935
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 9, Application PC/TUS9603935 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            179 HOCKISCESMGASKYRWFHNACCECIGPECIDYGSKTVKCMNC 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         164 NKCRQQCESMGASSYRWFHDGCCECVGENCLNYGINESRCRGC 206
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                              TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Iocal Similarity 35.4%;
hes 79; Conservation
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LEGGTH: 206 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MQLLCYFVILFVGIAPW-SSLANDDGCNEVVCGSVVSKCLITQSCQCKLND--CHCCKDC 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MKLH+YVAVLTLAILMFLTWLPESLSCNKALCASDVSKCLIQELCQCRPGEGNCSCCKEC 59
                                                                           REFERENCE/DOCKET NUMBER: 32
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                   STREET: 0 L.
STREET: 0 L.
CITY: ROSELAND
CTATE: NEW JERSEY
                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: CALLARY & CLARA ADDRESSEE: STEWART & CLARA ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: HUI NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
SEQUENCE CHARACTERISTICS:
LENGTH: 206 amino acids
                                                                                                                                         CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                             NAME: Ferraro, Gregory D
REGISTRATION NUMBER: 36,
                                                                                                                                                                             APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                        COUNTRY: USA
ZIP: 07068-1739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: si
TOPOLOGY: linear
                                                              TELEPHONE:
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                                                              201-994-1700
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Pred. No. 5.34e-46;
55; Mismatches 70; Indels 1
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RESULT ID US

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SEQUENCE

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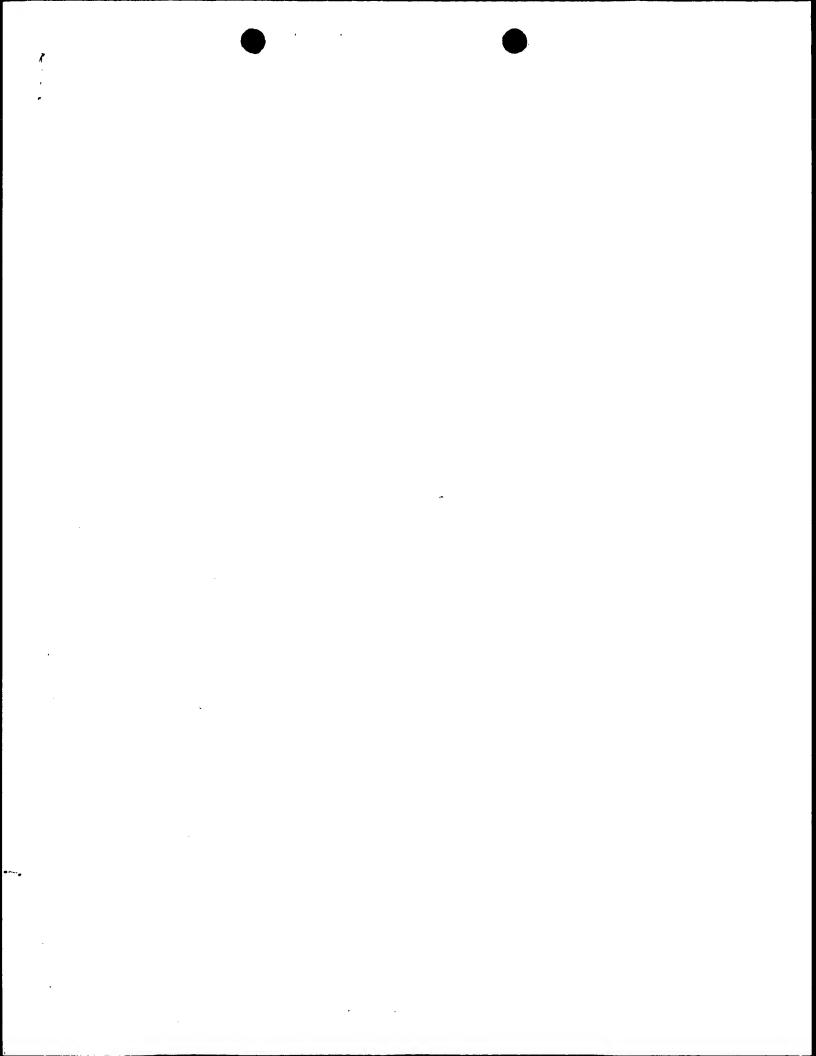
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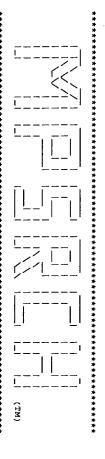
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 9, Application US/09416267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 9, Application US/09416267 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                119 VSFPVAEELSHHENLVSFLETVNQPHHQNVSVPSNNVHAPYSSDKEHMCTVVYFDDCMSI 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               115 IRFSMRAGFKQR---VA--QG-GAS--GDAGNGNGNGNAG-SAGVT-LCTVIY-NSCIRA 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            179 HQCKISCESMGASKYRWFHNACCECIGPECIDYGSKTVKCMNC
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                                         TELEFAX: 301-309-000 9: INFORMATION FOR SEQ ID NO: 9: SEQUENCE CHARACTERISTICS: LENGTH: 206 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Jacal Similarity 35.4%; les 79; Conservation
                                                                                                  ATTORNEY/AGENT INFORMATION:

NAME: JOSEPH J. KENNY
REGISTRATION NUMBER: 43,710
REFERENCE/DOCKET NUMBER: PF27/
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/416,267
FILING DATE: OCT-12-199
CLASSIFICATION: 435
CCLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: LI, YI
APPLICANT: SU, KUI
APPLICANT: SU, KUI
APPLICANT: LI, HADDONG
TITLE OF INVENTION: HUMAN CYTOKINE POLYPEPTIDE
NUMBER OF SEQUENCES: 9
                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MLCLGALWDECCDCVGMCNPRNYSDTPP-TSKSTVEELHEPIPSLFRALTEGDTQLNWNI 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MKLH-YVAVLTLAILMFLTWLPESLSCNKALCASDVSKCLIQELCQCRPGEGNCSCCKEC 59
MOLECULE TYPE: protein
            STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                       COUNTRY: UZIP: 20850
                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Human Genome Sciences, Inc
STREET: 9410 Key West Avenue
CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LE TYPE: protein
206 AA; 22216 MW; 187648 CN;
                                     amino acid
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                                                                                                                                                                                                                                                                                                                    USA
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                       single
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                                                                                                                               PF270P1
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Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
179
                    164 NKCRQQCESMGASSYRWFHDGCCECVGENCLNYGINESRCRGC 206
                                                                       119
                                                                                                         115 IRFSMRAGFKQR---VA--QG-GAS--GDAGNGNGNGG-SAGVT-LCTVIY-NSCIRA 163
                                                                                                                                               60 MLCLGALWDECCDCVGMCNPRNYSDTPP-TSKSTVEELHEPIPSLFRALTEGDTQLNWNI 118
                                                                                                                                                                                 58 LNCLGELYIECCGCLDMC-PKHKDVLPSLTPRSEIGDI-EGVPELFDTLTAEDDE-GWST 114
                                                                                                                                                                                                                                        1 MQLLCYFVILFVGIAPW-SSLANDDGCNEVVCGSVVSKCLITQSCQCKLND--CHCCKDC
                                                                                                                                                                                                                     1 MKLH-YVAVLTLAILMFLTWLPESISCNKALCASDVSKCLIQELCQCRPGEGNCSCCKEC
HQCKISCESMGASKYRWFHNACCECIGPECIDYGSKTVKCMNC
                                                                       VSFPVAEELSHHENLVSFLETVNQPHHQNVSVPSNNVHAPYSSDKEHMCTVVYFDDCMSI 178
                                                                                                                                                                                                                                                                                                                                                                  206 AA; 22216 MW; 187648 CN;
                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                            31.2%;
                                                                                                                                                                                                                                                                                       Score 542; DB 20; I
Pred. No. 5.34e-46;
55; Mismatches 70;
                                                                                                                                                                                                                                                                                                                             Length 206;
                                                                                                                                                                                                                                                                                           Indels 19;
                                                                                                                                                                                                                                                                                           Gaps 14;
                                                                                                                                                                                                                   59
                                                                                                                                                                                                                                                       57
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Search completed: Wed Aug 16 09:40:22 2000 Job time: 277 secs.





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rch\_pp protein - protein database search, using Smith-Waterman algorithm

on: Wed Aug 16 09:29:10 2000; MasPar time 7.85 Seconds 672.622 Million cell updates/sec

**Tabular** output not generated.

Title: Description: (1-223) from US09416267.pep 1738 >US-09-416-267-2

Sequence: Perfect Score: 1 MKLHYVAVLTLAILMFLTWL.....IGPECIDYGSKTVKCMNCMF 223

Scoring table: рам 150 Gap 11

188963 seqs, 23686106 residues

Post-processing: Minimum Minimum Match 0% Listing first 45 summaries

Database: a-geneseq36 1:geneseqp

Statistics: Mean 32.312; Variance 138.507; scale 0.233

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result	Score	% Query Match	Length	BG			Pred. No.
1	1738	100.0	223	_ ;	W32112	A novel human cytokine	8.73e-158
N	1738	100.0	223	ب	59	Human growth factor Ta	15
w	100	5.8	420	_	Y13362	quence	.28e+
4	100		420	μ.	Y05281	EGF-like homologue PRO	•
ر.	97		3084	ᆫ	P94758	of mouse l	
σ	95		77	ب	W94641		
7	95		122	Ц	W52271	Truncated soluble tumo	
· œ	95		183	Н	R77421	BamTP delta53 nerve gr	1.93e+01
9	95	•	235	Н	W52270	is fac	
10	95		235	$\vdash$	W59665	Human soluble tumour n	
11	95	٠	235	ب	W89234	Tumour necrosis inhibi	1.93e+01
12	95		461		R72504	p75 Tumour Necrosis Fa	
13	95	٠	461	ш	R11001	40kD TNF inhibitor pre	1.93e+01
14	95		461	ш	R11141	Human TNF-R deduced fr	1.93e+01
15	95		461	L	R42058	Fibroblast derived TNF	1.93e+01
16	95	5.5	485	<u></u>	R24016	Fusion protein INFRFc.	1.93e+01
17	95		1453	_	R27820	CCV-C54 spike protein.	:
18	96		1801	μ	W50895	nin Bi	٠
19	96		3084	<b>~</b>	W50891	Mouse laminin A chain.	1.63e+01
20	93	5.4	392	Н	R11605	Human 75kD TNF-binding	٠
21	93	5.4	518	Ь	R51003	Sequence of a recombin	2.71e+01
22	93	5.4	1454	_	R42473	FIPV/FECV chimeric spi	
23	93	5.4	1454	ר	R42475		-

Query Match 100.0%; Best Local Similarity 100.0%; Matches 223; Conservative

Score 1738; DB 1; Pred. No. 8.73e-158; 0; Mismatches 0;

Length 223; Indels

0

Gaps

0

Query Match Best Local S

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24
86	86	87	89	88	89	89	89	89	89	89	89	68	89	89	89	90	91	91	94	93	93
4.9	4.9	5.0	5.1	5.1	5.	5.1	5.	5.1	5.1		٠	٠	5.1	5.1		5.2				5.4	5.4
405	56	326	1964	1483	1454	381	381	326	326	326	326	326	326	326	194	925	54	53	3075	1454	1454
					-	<b>ب</b> ـــو	<u>ب</u>	<u>۔</u>	<u>ــر</u>	ᆫ	ᆫ	بر	ب	ы	<b>_</b>	<b></b>	щ	щ	سر	Ь	ш
Y04128	R15316	R22007	W95557	P80474	R24511	W35730	W35957	W82311	R87655	R41524	R47386	R45744	R93989	R84192	R45743	R79148	R14329	R15319	W50892	R42477	R42468
Pseudomonas putida cyt	Epithelin, growth modu	'n	Mus musculus notch4 pr	Sequence of protein of	genon	Human cysteine rich pr	Human monocyte mature	Human Al adenosine rec	Human adenosine recept	Human Al adenosine rec	Human Al adenosine rec	Human Al adenosine rec	Human ventricle Al ade	Human Al adenosine rec	Human Al adenosine rec	Human insulin receptor	Epithelin, growth modu	Epithelin, growth modu	Human laminin A chain.	FECV/FIPV chimeric spi	Feline enteric coronav
8.56e+01			5.25e+01	6.18e+01	5.25e+01	5.25e+01	5.25e+01		•	5.25e+01	5.25e+01	5.25e+01	5.25e+01	5:25e+01	5.25e+01	4.45e+01	3.77e+01	3.77e+01	2.29e+01	2.71e+01	2.71e+01

#### ALIGNMENTS

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W32112 standard; Protein; 223 AA.

W32112;
06-APR-1998 (first entry)
A novel human cytokine with homology to the Drosophila TSG product.
Cytokine; Drosophila twisted gastrulation gene product; TSG;
Cytokine; Drosophila twisted gastrulation gene product; TSG;
                                                    The present sequence represents a novel human cytokine, which has a high degree of similarity to the Drosophila twisted gastrulation gene (TSG) product. Compounds which bind to and inhibit activation of the the cytokine protein can be identified in the following manner. Cells expressing a receptor for the present cytokine on the surface are contacted with an analytically detectable cytokine, and the test compound, under conditions which permit binding to the receptor. The absence of a signal generated from the interaction of the cytokine with the receptor indicates whether the test compound binds to and inhibits the receptor. The diagnosis of a disease related to under-expression of the cytokine comprises determining a mutation in the DNA encoding the cytokine. This DNA, or the cytokine plypeptide. Inhibitors of the
                  cytokine can also be used to treat patients in need of a cytokine inhibitor.
                                                                                                                                                                                                                                                                                                          Claim 15; Page 58; 73pp; English.
                                                                                                                                                                                                                                                                                                                                              DNA encoding human cytokine with homology to Drosophila twisted gastrulation gene product - useful in research, diagnostic and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO9734998-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cytokine inhibitor.
                                                                                                                                                                                                                                                                                                                                clinical arts
                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; T88982.
                                                                                                                                                                                                                                                                                                                                                                                                                            (HUMA-) HUMAN GENOME SCI INC.
Li H, Li Y, Su K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20-MAR-1996; U03935.
20-MAR-1996; WO-U03935.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               inhibition; activation; cytokine under-expression; disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25-SEP-1997
                                                                                                                                                                                                                                                                                                                                                                                                      , Li Y, Su K;
97-480207/44.
    223
  ΑĄ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "mature protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1. .20
/note= "signal peptide"
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Š 밁 Qγ

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PT New isolated growth factor, Tango-67 - used to develop products for the disgnosis and treatment of inflammation or disorders associated PT with cellular proliferation
PS Claim 5; Fig 1; 69p; English.
CC growth factor which is capable of promoting cell proliferation
CC and/or differentiation. The sequence was deduced from the concelled provide sequence (see v63465) of a cDNA clone obtained from a nucleotide sequence (see v63465) of a cDNA clone obtained from a clone obtained from a clone astrocyte cDNA library. Tango-67 is related to a number of complete acid molecules and polypeptides, host cells, vectors and concelled acid molecules and polypeptides, host cells, vectors and disorders associated with aberrant expression or activity of tango-67. In particular they can be used for the treatment of inflammation or disorders can be used to diagnose or treat concentration. The products can be used in wound healing, tissue products can also be used for detection, diagnosis and screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-FEB-1999 (first entry)
Human growth factor Tango-67.
Tango-67; growth factor; human; inflammati
therapy; diagnosis; wound healing; tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
WO9846641-A1.
                                      181
                                                                             121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; V63465.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Holtzman D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                W70591 standard;
                                                                                                                        121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (MILL-) MILLENNIUM BIOTHERAPEUTICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            l5-APR-1998; U07603.
l6-APR-1997; US-843651.
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                                                                                                                                                                                                                                                                                                                                                                 Local
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                                                                                                                                                                                                                                                                        1 MKLHYVAVLTLAILMFLITWLPESLSCNKALCASDVSKCLIQELCQCRPGEGNCSCCKECM 60
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                             CKISCESMGASKYRWFHNACCECIGPECIDYGSKTVKCMNCMF
                                                                                             EPVAEELSHHENLVSFLETVNQPHHQNVSVPSNNVHAPYSSDKEHMCTVVYFDDCMSIHQ 180
                                                                                                                                                                                   LCLGALWDECCDCVGMCNPRNYSDTPPTSKSTVEELHEDIPSLFRALTEGDTQLNWNIVS 120
                                                                    FPVAEELSHHENLVSFLETVNQPHHQNVSVPSNNVHAPYSSDKEHMCTVVYFDDCMSIHQ
                                                                                                                                                                                                                                            MKLHYVAVLTLAILMFLTWLPESLSCNKALCASDVSKCLIQELCQCRPGEGNCSCCKECM 60
LCLGALWDECCDCVGMCNPRNYSDTPPTSKSTVEELHEPIPSLFRALTEGDTQLNWNIVS 120
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                                                                                                                                                                                                                                                                                                                                       100.0%;
1 Similarity 100.0%;
223; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                223
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                                                                                                                                                                                                                                                                                                                                     Score 1738; DB 1;
Pred. No. 8.73e-158;
0; Mismatches 0:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8
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ng; tissue repair; vulnerary.
                                                                                                                                                                                                                                                                                                                                                                              Length 223;
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                      24-NOV-1997;
(GETH ) GENEN
Chen J, Godda
WPI; 99-22953
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31-OCT-1
31-OCT-1
03-NOV-1
07-NOV-1
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29-0CT-1
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17-OCT-1997
17-OCT-1997
17-OCT-1997
24-OCT-1997
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28-OCT-199
28-OCT-199
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29-OCT-199
                                                                                                                                                                                                                                                               12-NOV-19
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                                                                                                                                                                                                                                            18-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-JUN-1999 (first entry)
Amino acid sequence of protein PRO214.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Y13362
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25-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181 CKISCESMGASKYRWFHNACCECIGPECIDYGSKTVKCMNCMF 223
                    TH ) GENENTECH I
n J, Goddard A,
; 99-229533/19.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             standard;
                                                                                                      US-062814

US-063120

US-063120

US-063121

US-063121

US-063128

US-063541

US-063541

US-063542

US-063544

US-063544

US-063544

US-063544

US-063544

US-063744

US-063714

US-063714

US-063714

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US-064248

US-064248

US-065846

US-065846

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US-066372

US-0663120

US-0663146

US-066372

US-0663146

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US-0663164

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                                                                                      US-066453.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Protein; 420
                                        Gurney AL, Pennica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ₹
                                        á
                                      Wood WI,
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CARABBARB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ននិនិនិនិន
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cc associated with the preservation and maintenance of gastrointestinal comucosa and the repair of acute and chronic mucosal lesions (e.g. enterocolitis, Zollinger-Ellison syndrome, gastrointestinal cc (le.g. enterocolitis, Zollinger-Ellison syndrome, gastrointestinal cc ulceration and congenital microvillus atrophy), skin diseases associated cancers such as lung squamous cell carcinoma of the vulva and gliomas), cc potent effects on cell growth and development, diseases related to growth cc survival of nerve cells including Parkinson's disease, Alzheimer's disease, ALS, neuropathies or cancer. PRO265 can be used as for fibromodulin, e.g. for reducing dermal scarring. PRO264 can be used as a target for anti-tumor drugs. PRO253 may be used in the treatment cc anti-thrombotic agent; PRO287 polypeptides and portions may have cf therapeutic applications in wound healing and tissue repair; PRO317 can be used for treating problems of the kidney, uterus, endometrium, blood crossels, or related tissue, e.g. in the heart of genital tract.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                         25-NOV-1997; US-066840.

17-SEP-1997; US-059114.

17-SEP-1997; US-059117.

18-SEP-1997; US-059263.

15-OCT-1997; US-062285.

17-OCT-1997; US-062285.

17-OCT-1997; US-062287.

24-OCT-1997; US-062816.

29-OCT-1997; US-063704.
Antibodies against specific proteins overexpressed in tumours Example 1; Fig 10; 130pp; English.

This sequence represents the EGF-like homologue PRO214.

The invention relates to antibodies (Ab) that bind to any of the polypeptides (I) designated PRO187; PRO533; PRO214; PRO240; PRO211; PRO230; PRO261; PRO246 or EBAF-2. The Ab, or other agents that inhibit expression and/or activity of (I) are used: (i) to inhibit growth of tumours; and (ii) as diagnostic/prognostic reagents for detection or quantification of (I) in cells or tissues, by standard immunoassays, with overexpression being indicative of cancer. For therapeutic use, the Ab may be conjugated to a toxin, chemotherapeutic agent or radioisotope. Genes expressing (I), many of which are growth factor homologues, are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The CDNA sequences are obtained from cDNA libraries, prepared from fetal lung, fetal kidney, fetal brain, fetal liver and fetal retina. The encoded polypeptides have specific uses based on their homology to known polypeptides, e.g. PRO211 and PRO217 can be used for disorders associated with the preservation and maintenance of gastrointestinal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EGF-like homologue PRO214,
Antibody, PRO187; PRO533; PRO214;
EBAF-2; inhibitor; tumour growth;
                                                                                                                                                                                                                                                              N-PSDB; X28431.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO9914327-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Y05281 standard; Protein; Y05281;
                                                                                                                                                                                                                                                                                                                 Roy M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gastrointestinal ulceration Claim 12; Fig 40; 320pp; English
                                                                                                                                                                                                                                                                                                                                                       (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Y13344-403 represent secreted and transmembrane human proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated human genes and polypeptides used in, e.g. treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 236 WALHHLKCVDIDECGTEGANCGADQFCVNTEGSYECRDCAKACLGCMGA 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5.8%;
Local Similarity 28.6%;
nes 14; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -SEP-1998; U18824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WLPESISC-NKALCASDVSKCLIQELCQCRPGEGNC-SCCKECMLCLGA 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          homologue.
                                                                                                                                                                                                                                                                                                                 Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     420 AA;
                                                                                                                                                                                                                                                                                                                                      Goddard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                 A, Gurney
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 100; DB 1; Le
Pred. No. 8.28e+00;
12; Mismatches 21;
                                                                                                                                                                                                                                                                                                                                 A, Hillan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRO240; cancer;
                                                                                                                                                                                                                                                                                                                                   K, Lawrence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRO211; PRO230; PRO261; PRO246; EGF-like homologue;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 5.6%;
Best Local Similarity 40.0%;
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 5.8%;
Best Local Similarity 28.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                               29-APR-1999 (first entry)
TNF-R extracellular Cys-rich domain TNF-R p75.
TUNF-R extracellular Cys-rich domain TNF-R; autoimmune diseases;
Tunour necrosis factor receptor; TNF-R; autoimmune diseases;
inflammation; septic shock; cachexia; graft versus host disease;
skin allergic reaction; immune complex disease; malaria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          peptide
protein
Disclosure; Fig 1; 78pp; English.

The present invention describes peptides and peptide analogues which correspond in primary sequence to a binding loop of a tumour necrosi
                                                New compounds designed from a binding loop of a tumour necrosis factor receptor - are capable of inhibiting the biological activities of tumour necrosis factor, e.g., in treating inflammation or autoimmune diseases
                                                                                                             30-MAY-1997; US-866545.
(UYPE-) UNIV PENNSYLVANIA.
Greene MI, Murali R, Takas:
WPI; 99-080781/07.
                                                                                                                                                                                                                                                                                                                                                                                                                                          1091 FPDCLPCPCHLTPTLPHTCDLEQGLCSCSEDSGTCSC-KE 1129
                                                                                                                                                                         03-DEC-1998; U10891.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The sequence encoding mouse laminin A chain (N91779) is used as a probe to screen a human cDNA library. Laminin is a very potent and rapid stimulator of neurite outgrowth and promotes both central and periphera.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (USSH) US Dept Health & Humar
Yamada Y, Sasaki M, Kleinman
WPI; 89-138175/18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P94758;
27-JAN-1991 (first entry)
Sequence of mouse laminin A chain
                                                                                                                                                                                                           W09853842-
                                                                                                                                                                                                                                                                                                                                                 W94641 standard; peptide; 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nerve regeneration.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA encoding human laminin A chain, used in vector system and new synthetic peptide(s) with laminin-type biological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              07-NOV-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 T 5
P94758 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        overexpressed in some cases of cancer
                                                                                                                                                                                                                             OHOHO
                                                                                                                                                                                                                                       transplantation rejection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Figure 4; 90pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; N91779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US7267564-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Peripheral nerve regeneration.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-FEB-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            236 WALHHLKCVDIDECGTEGANCGADQFCVNTEGSYECRDCAKACLGCMGA 284
                                                                                                                                                                                                                                                                                                                                                                                                             20 LPESLSCNKALCASDVSKC-LIQELCQCRPGEGNCSCCKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19 WLPESLSC-NKALCASDVSKCLIQELCQCRPGEGNC-SCCKECMLCLGA 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           420 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3084 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-267564.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein; 3084 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .3084
                                                                                                                               Takasaki W;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            & Human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 97; DB 1; Len
Pred. No. 1.38e+01;
5; Mismatches 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 100; DB 1;
Pred. No. 8.28e+00
                                                                                                                                                                                                                                                                                                                                                 B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HK, Martin GR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              used in vector system
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 3084;
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                                                                                                                                                                                                                                                                   host disease;
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PR
Truncated and soluble forms of tumour necrosis factor receptor receptor is useful for treating diseases involving factor, e.g. arthritis and production of treating diseases syndrome adult respiratory distress syndrome claim 3; page -; 205p; English.

CC This sequence is a truncated soluble tumour necrosis factor receptor cc (sTNFR) protein of the invention. The truncated sTNFR proteins and tumour necrosis factor binding proteins (TNBP) are used to treat any stream of the invention, and the syndrome, graft crystore, cachexia/anorexia, cancer, chronic fatigue syndrome, graft crystore, alzheimer's disease and other autoimmune diseases. Cells crystorme, cachexia/anorexia, cancer, chronic fatigue syndrome, graft crystorme, cachexia/anorexia, cancer, which may also be used for measuring the amount of sTNFR in samples and to raise antibodies against sTNFR. Crystormed with seed in preparation of therapeutic compositions for treating the above diseases. The sTNFR proteins are well suited to large call production (since they lack the deamidation site in region 111-126, so are more stable in vivo); contain fewer disulphide bonds and fewer ceptopes, making them less antigenic than full-length proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local S
Matches 2
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04-MAR-1997; US-039792,

09-JUL-1996; US-021443,

06-DEC-1996; US-023534,

23-JAN-1997; US-037737,

07-FEB-1997; US-039314.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Truncated soluble tumour necrosis factor receptor. Soluble tumour necrosis factor receptor; STNFR; TNF-mediated disease; Soluble tumour necrosis factor binding protein; autoImmune disease; arthritis; adult respiratory distress syndrome; cachexia/anorexia; cancer; therap; chronic fatigue syndrome; graft rejection; Alzheimer's disease; TNBP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           factor receptor (TNF-R) superfamily member. The compounds are especially designed from a binding loop of TNF-R p55. They are capable of inhibiting TNF binding to its cellular receptors and may be used to inhibit the biological activities of TNF. They may be used in treating TNF-associated conditions such as acute and chronic inflammatory responses, septic shock, cachexia, autoimmunity, graft-versus-host disease, skin allergic reactions, immune complex disease, cachexia, autoimmunity graft-versus-nost transplantation rejection and malaria. Administration is, e.g. oral, transdermal, transmucosal, pulmonary, subcutaneous, intravenous or intramuscular. Parenteral dosage is 0.15 mg/kg/day. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                             (AMGE-) AMGEN INC.
Edwards CK, Fisher EF, Kieft GL;
WPI: 98-101052/09.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequence represents an extracellular Cys-rich domain of TNF-R from the present invention.

Sequence 77 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "optionally deleted"
Misc_difference 32. .115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Misc_difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ney Location/Qualifiers Misc_difference 1. .31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               W52271 standard; Protein; 122 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO9801555-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29-JUN-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5-JAN-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16 WVPECLSCG-SRCSSDQVETQACTREQNRICTCRPG-WYCALSKQEGCRLC-APLRK-C 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Match 5.5%;
Local Similarity 42.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19 WLPESLSCNKALCASD-V-SK-CLI-QE-LCQCRPGEGNCSCCK-E-CMLCLGALWDEC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "residues 32-115 of human
116. .122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "optionally deleted"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10; Mismatches 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           95; DB 1;
No. 1.93e+01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TNF inhibitor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      therapy;
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Query Match Best Local S

Local Similarity

42.48;

Score Pred.

No.

Length 122

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Best Local
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                                                                                                                                                  09-JUL-1997; U12244.

04-MAR-1997; US-039792.

09-JUL-1996; US-021443.

06-DEC-1996; US-032534.

23-JAN-1997; US-037737.

07-FEB-1997; US-039314.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-NOV-1995;
02-MAY-1995;
09-MAY-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               differentiation of nerve and gilal cells.

Example 1; Page 36-37; 57pp; English.

The synthetic nerve growth factor (NGF) gene isolated from Bam TP delta 53 plasmid pr3XI-2 is designed to optimize codons for expression in Escherichia coli as well as create unique sites for subsequent cloning steps. The recombinant protein is solubilized and sulfonylated and allowed to refold in the presence of PEG and urea. Biologically active NGF, used for promoting the survival of and mintaining the phenotypic differentiation of nerve and gilal cells, is isolated and purified. This method breaks incorrectly formed disulphide bonds and allows refolding of the factor into the correct tertiary structure required for maximum yield of full active mortain.
                             (AMGE-) AMGEN INC.
Edwards CK, Fisher EF, Kieft
WPI; 98-101052/09.
N-PSDB; V19802.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Tumour necrosis factor inhibitor.
Soluble tumour necrosis factor receptor; STNFR; TNF-mediated disease;
tumour necrosis factor binding protein; autoimmune disease; arthritis;
adult respiratory distress syndrome; cachexia/anorexia; cancer; therap
tumour necrosis factor inhibitor; Alzheimer's disease; TNBP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   W52270 standard; Protein; 235 AA. W52270; 29-JUN-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bonam D, Kohno T, WPI; 95-404080/51.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R77421 standard; Protein; 183 R77421;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                active protein.
Sequence 183 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; T05443.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein refolding; NGF; plasmid pT3XI-2.
                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens. WO9801555-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27-JUN-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10-FEB-1996 (first entry)
Truncated and soluble forms of tumour necrosis factor receptor
                                                                                                                                                                                                                                                                                                                                                   L5-JAN-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 useful for promoting the survival and maintaining phenotypic
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les 25; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WLPESLSCNKALCASD-V-SK-CLI-QE-LCQCRPGEGNCSCCK-E-CMLCLGALWDEC 70
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5.5%;
larity 42.4%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10;
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Pred. No. 1.93e+01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rosendahl MS;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   was used to make the truncated soluble tumour necrosis factor receptor (STNFR) proteins of the invention. The truncated sTNFR proteins and tumour necrosis factor binding proteins (TNBP) are used to treat any TNF-mediated disease, e.g. arthritis, adult respiratory distress syndrome, cachexia/anorexia, cancer, chronic fatigue syndrome, graft rejection, Alzhelmer's disease and other autoimmune diseases. Cells transformed with a vector containing DNA encoding the protein may be used for production of recombinant sTNFR, which may also be used for measuring the amount of STNFR in samples and to raise antibodies against sTNFR. TNBP may also be used in preparation of therapeutic compositions for treating the above diseases. The STNFR proteins are well suited to large scale production (since they lack the deamidation site in region 111-126, so are more stable in vivo); contain fewer disulphide bonds and fewer scause production (since they lack the deamidation site in region 111-126, so are more stable in vivo); contain fewer disulphide bonds and fewer scause production.
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Matches 2
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Best Local Similarity 42.4%;
Matches 25; Conservative
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09-UUL-1997; US-052023.
06-DEC-1996; US-032587.
23-UAN-1997; US-036355.
07-FEB-1997; US-039315.
                                  W89234 standard; Protein; 235
W89234;
04-MAR-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                               one additional anti-inflammatory drug, e.g. methotrexate Disclosure; Fig 2; 104pp; English.
This is the amino acid sequence of the human tumour necrosis factor receptor type II, used in the method of the invention involving the treatment of acute or chronic inflammatory disease such as leukaemia by administering tumour necrosis factor binding protein and at least one additional anti-inflammatory drug, e.g. methotrexate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Treatment of acute or chronic inflammatory disease, e.g. leukaemia by administering tumour necrosis factor binding protein and at leas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (AMGE-) AMGEN INC.
Bendele AM, Edwards CK, Sennello RM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human soluble tumour necrosis factor receptor type II. Human; tumour necrosis factor; TNF; TNF receptor type II; inflammatory disease; leukaemia; TNF binding protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             useful for treating diseases involving factor, e.g. arthritis and adult respiratory distress syndrome Claim 3; Fig 8; 205pp; English.
This sequence is the human tumour necrosis factor inhibitor. The protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; V41549
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W09824463-A2.
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Local Similarity 42.4%;
hes 25; Conservati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               67 WYPECLSCG-SRCSSDQYETQACTREQNRICTCRPG-WYCALSKQEGCRLC-APLRK-C 121
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                                                                                                                                                                                                                                                                                                                                    235 AA;
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10; M
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Pred. No. 1.93e+01
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                                                                                                                                                                                                                                                                     DB 1;
1.93e+01
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13; Indels 11;
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                                                                                                                                                                                                                                                  Indels 11;
at least
                                                                                                                                                                                                                                               Gaps
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RESULT.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PT New Chimeric Osteoprotegerin polypeptides - contain the PT osteoprotegerin dimerisation domain and a heterologous sequence, PT useful to treat TNF and TNFR-mediated disorders PS Disclosure; Fig 3; 92pp; English.

CC The present invention describes a chimeric polypeptide (A1), comprising CC annoacid sequence. Also described are: (1) a multimer polypeptide (CC amino acid sequence. Also described are: (2) an isolated nucleic acid encoding A1; (3) an expression vector comprising the nucleic acid sequence; and (4) a host cell transformed or transferted with the CC expression vector so that the nucleic acid is expressible. The products CC from the present invention are useful to treat a variety of disorders CC including those related to receptor binding. Compositions comprising CC undour necrosis factor (TNF)/OPG and TNF receptor (TNF)/OPG chimeras CC are used to treat TNF and TNFR-mediated disorders such as inflammation, CC autoimmune diseases and disorders related to excessive apoptosis. The CC insertain and constant sequences to identify potential new receptors and CC ligands. The present sequence represents the TNF inhibitor 40 kDa and CC interests.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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WO9849305-A1.
05-NOV-1998.
Tumour necrosis factor (TNF) receptor ligand - used to increase inhibitory effect of a soluble TNF receptor Disclosure; Figure 2; 18pp; English.
A ligand to a member of the tumour necrosis factor (TNF)/nerve growth factor (NGF) receptor family which binds either to the r
                                                                                                                                                                                                                                  12-OCT-1993; IL-107267.

(YEDA ) YEDA RES & DEV CO LTD.

(WALL) WALLACH D.

ROJECTOR
                                                                                                                                                                                   Beletsky I, Bigda
WPI; 95-148673/20.
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Tumour necrosis factor receptor 1; TNFR-1; inhibitor; osteoprotegerin; OPG; chimeric; fusion; dimerisation domain; autoimmune disease;
                                                                                                                                                                                                                                                                                                                                                                                                         EP-648783-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     misc_difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31-OCT-1995 (first entry) p75 Tumour Necrosis Factor Receptor.
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N-PSDB; V81733.
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Boyle WJ, Wooden S;
                                                                                                                                                            N-PSDB; Q89544
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ligand; tumour necrosis factor; nerve growth factor; TNF; NGF;
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01-MAY-1997; US-850188.
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Similarity 42.4%;
25; Conservation
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                                                                                                                                                                                                                                                                                                                                            116015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /label= Transmembrane domain.
259
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "Unidentified amino acid."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label- TBPII.
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Pred. No. 1.93e+01;
10; Mismatches 13
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                                                                                                                      to increase
   the region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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11;

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PR 1111
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ID RI
AC RI
DT 11
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24-JAN-1991.
16-JUL-1990; 058976.
18-JUL-1989; US-381080.
11-DEC-1989; US-450329.
07-FEB-1990; US-479661.
20-MAR-1991.
10-SEP-1990;
11-SEP-1989;
13-OCT-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tumour necrosis factor inhibitor - for suppression of TNF-alpha and -beta, useful as therapeutic agent.

Disclosure; Fig 39; 142pp; English.

The sequence comprises the entire 40 kD TNF inhibitor. The clone from which the sequence was deduced was isolated from a cDNA library prepd. from RNA form U37 cells treated with PMA/PHA. The whole gene can be inserted into expression vectors for prepn. of TNF inhibitor for use in the treatment of inflammatory and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 of the 4th-Cys rich domain of the receptor, or to the region between it and the cell membrane may be used in the production of a pharmaceutical composition for increasing the inhibitory effect of a soluble receptor of the TNF/NGF receptor family. This sequence is the sequence of the p75 TNF receptor.
                                                                                                                                                                                                                                                                                                                                                                      R11141 standard;
R11141;
                                                                                                                                                                                                                                                Key
                                                                                                                                                                                                                                                                                                                          24-MAY-1991 (first entry)
Human TNF-R deduced from clone 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
AU9058976-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tumour necrosis factor; inhibitor.
                                                                                                EP-418014-A.
                                                                                                                                                                              protein
                                                                                                                                                                                                                        peptide
                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                   cachexia; septic shock.
                                                                                                                                                                                                                                                                                                        Tumour necrosis factor receptor;
                                                                                                                                                                                                                                                                                                                                                  24-MAY-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   degenerative diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; Q10907
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (SYNE-) SYNERGEN INC. WPI; 91-073847/11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     40kD TNF inhibitor precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13-MAY-1991 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R11001 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               89 WVPECLSCG-SRCSSDQVETQACTREQNRICTCRPG-WYCALSKQEGCRLC-APLRK-C 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WLPESLSCNKALCASD-V-SK-CLI-QE-LCQCRPGEGNCSCCK-E-CMLCLGALWDEC 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         h 5.5%;
Similarity 42.4%;
25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R10986 and R10984.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              461 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      461 AA;
             309875.
US-405370.
US-421417.
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                                                                                                                                       /label= TNF receptor 258. .287
                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                    /label= signal sequence
                                                                                                                                                                                                                                                                                                                                                                                         Protein; 461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protein;
                                                                                                                   /label=
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                                                                                                                                                                                .461
                                                                                                                 transmembrane region
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Pred. No. 1.93e+01
10; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 95; DB 1; I
Pred. No. 1.93e+01;
10; Mismatches 13
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                                                                                                                                                                                                                                                                                                        immune response; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 461;
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The sequence was deduced from a DNA sequence obtd. from a clone isolated from a library prepd. from a human fibroblast cell line, WI-26 VA4 (ATCC CCL 95.1). The clone is deposited as Accession N 68088 under the name pcAV/NOT-TNF-R. The DNA can be truncatd to produce sequences which express soluble receptor comprising residues 1-235, 1-185 or 1-163 of the protein.
  New fusion protein tumour necrosis factor and human interleukin-1 receptor - useful in therapy, diagnosis and assays of e.g. rheumatoid arthritis, diabetes, cerebral malaria, sepsis, etc. Claim 5; Fig 2; 85pp; English.

The sequences given in R42058-59 repressent human tumour necrosis factor receptor (TNF-R) and the sequences in R42060-61 represent human interleukin-1 receptor (IL-IR). These sequences were used in the sequences which were the sequences where the sequences were used in the sequences which were the sequences which were the 
                                                                                                                                                                                                                                                                                                                                                                                     peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; tumour necrosis factor receptor; TNP-R; interleukin-1 receptor; IL-IR; fusion protein; linker; TNF; IL-1; cachexia; cerebral malaria; rheumatoid arthritis; diabetes; multiple sclerosis; septic shock; pulmonary fibrosis; silicosis; allograft; xenograft; rejection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  בי-ארא־ביא (first entry) Fibroblast derived TNF-R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; Q10990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (IMMU-) IMMUNEX CORP.
Smith CA, Goodwin RG, Beckmann PM;
WPI; 91-082230/12.
                                                                                                                                                        N-PSDB;
                                                                                                                                                                                                  Smith
                                                                                                                                                                                                                                           26-MAR-1993;
30-MAR-1992;
                                                                                                                                                                                                                                                                                                        WO9319777-A.
                                                                                                                                                                                                                                                                                                                                           peptide
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                                                                                                                                                                                                                     (IMMV ) IMMUNEX CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1990; US-523635.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5.5%;
Similarity 42.4%;
                                                                                                                                                        049931
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US-860710.
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23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          . 206
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                                                                                                                                                                                                                                                                                                                                                                 "Preferred
                                                                                                                                                                                                                                                                                                                                                                                                         "Preferred
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Preferred soluble TNF-R"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Signal peptide"
                                                                                                                                                                                                                                                                                                                          "Preferred
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Preferred soluble TNF-R"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Preferred soluble TNF-R"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Mature hTNF-R"
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Pred. No. 1.93e+01
10; Mismatches 1
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                                                                                                                                                                                                                                                                                                                          soluble
                                                                                                                                                                                                                                                                                                                                                                 soluble TNF-R"
                                                                                                                                                                                                                                                                                                                                                                                                         soluble TNF-R"
                                                                                                                                                                                                                                                                                                                                                                                                                                                  soluble TNF-R"
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CC the production of a fusion protein which conformed to one of the CC formulae:
CC TNFT-R-linker-TNF-R-linker-TNF-R or IL-1R-linker-TNF-R-linker-TNF-R or CC TNFT-R-linker-TNF-R or TNF-R-linker-TNF-R or TNF-R-linker-TNF-R or TNF-R-linker-TNF-R or These linkers separate the individual moeities compared by such a distance that each component of the fusion protein is compared by such a distance that each component of the fusion protein is compared by the secondary or tertiary structure required for its biological activity. These fusion proteins may be used in cc capable of folding into the secondary or tertiary structure required for its biological activity. These fusion proteins may be used in cc capable of folding into the secondary for conditions may be used in cc capable of the secondary in capable of conditions in which both TNF and IL-1 play a causitive role. They may be used to treat cachexia, rheumatoid arthritis, cc diabetes, multiple sclerosis, pulmonary fibrosis and silicosis, cerebral malairia, allograff and xenograff rejection in graft verses autoimmune dysfunctions.
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Ouery Match
S.5%; Score 95; DB 1; Length 461;
Best Local Similarity 42.4%; Pred. No. 1.93e+01;
Matches 25; Conservative 10; Mismatches 13; Indels 11; Gaps 11;
Db 89 WVPECLSCG-SRCSSDQVETQACTREQNRICTCRPG-WYCALSKOEGCRIC-ADIRK-C 143

